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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:10:25; Search time 33.5 Seconds

(without alignments)

R71.18: US-10-084-507B-22

Prife: US-10-084-507B-22

Prife: US-10-084-507B-22

Prife: US-10-084-507B-22

Sequence: 1809
Sequence: 1 MGSLYSEYLNPNKVQEHYNY......LERGWHMPTSPTFLEGNTVV 353
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
```

Total number of hits satisfying chosen parameters: 572060

572060 segs, 82675679 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database: Issued\_Petents\_AA:\*

1: /cgn2\_c6/ptodata1/liaa/5\_COMB.pep:\*
2: /cgn2\_c6/ptodata1/liaa/H\_COMB.pep:\*
3: /cgn2\_c6/ptodata1/liaa/H\_COMB.pep:\*
4: /cgn2\_c6/ptodata1/liaa/PGTUS\_COMB.pep:\*
5: /cgn2\_c6/ptodata1/liaa/RE\_COMB.pep:\*
6: /cgn2\_c6/ptodata1/liaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|                            | Appli            | Appli            | Appl              | Appl              | Appli            | Appli            | Appl              | Appli            | Appli            | Appli           | Appl ,            | , Appl            | Appli           | Appli           | Appli            | Appli           | Appli           | Appli           | Appli           | , Appl            | , Appl           | , Appl            | , Appl            | , Appl           | Appli            | , Appl            | Appli           |
|----------------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|-------------------|------------------|------------------|-----------------|-------------------|-------------------|-----------------|-----------------|------------------|-----------------|-----------------|-----------------|-----------------|-------------------|------------------|-------------------|-------------------|------------------|------------------|-------------------|-----------------|
| ជ                          | 4,               | ý,               | 12,               | 13                | 'n               | 'n               | 10                | 'n               | 'n               | 'n              | 11,               | 24                | 7               | 'n              | 4,               | 4               | 4,              | 'n              | ĕ               | 28                | 18               | 28                | 17                | 18               | 4,               | 21                | 'n              |
| Description                | Sequence         | Sequence         | Sequence          | Sequence          | Sequence         | Sequence         | Sequence          | Sequence         | Sequence         | Sequence        | Sequence          | Sequence          | Sequence        | Sequence        | Sequence         | Sequence        | Sequence        | Sequence        | Sequence        | Sequence          | Sequence         | Sequence          | Sequence          | Sequence         | Sequence         | Sequence          | Sequence        |
| ID                         | US-09-582-200A-4 | US-09-582-200A-6 | US-09-582-200A-12 | US-09-731-030A-19 | US-09-582-200A-2 | US-09-582-200A-5 | US-09-582-200A-10 | US-09-274-752D-3 | US-08-196-989B-2 | US-08-760-936-2 | US-09-582-200A-11 | US-09-169-205D-24 | US-09-225-024-2 | US-09-262-477-2 | US-08-196-989B-4 | US-08-760-936-4 | US-09-225-024-4 | US-09-542-733-2 | US-08-845-566-3 | US-08-467-948A-28 | US-08-852-824-18 | US-08-467-947A-28 | US-09-731-030A-17 | US-09-518-383-18 | PCT-US96-10618-4 | US-09-169-205D-21 | US-09-082-088-2 |
| DB                         | 7                | 7                | 7                 | 7                 | ~                | N                | N                 | ~                | ч                | 7               | ~                 | N                 | ~               | ~               | Н                | Н               | N               | N               | Н               | Н                 | ~                | 7                 | ~                 | 0                | 4                | ~                 | N               |
| %<br>Query<br>Match Length | 353              | 353              | 353               | 353               | 353              | 353              | 353               | 353              | 352              | 352             | 352               | 352               | 352             | 382             | 383              | 383             | 383             | 382             | 381             | 381               | 381              | 381               | 381               | 381              | 381              | 382               | 378             |
| &<br>Query<br>Match        | 100.0            | 100.0            | 100.0             | 100.0             | 99.7             | 7.66             | 7.66              | 97.3             | 89.9             | 89.9            | 89.9              | 89.9              | 6.68            | 46.9            | 46.8             | 46.8            | 46.8            | 46.7            | 46.2            | 46.2              | 46.2             | 46.2              | 46.2              | 46.2             | 46.2             | 45.9              | 42.5            |
| Score                      | 1809             | 1809             | 1809              | 1809              | 1803             | 1803             | 1803              | 1760             | 1625.5           | 1625.5          | 1625.5            | 1625.5            | 1625.5          | 849             | 847              | 847             | 847             | 845             | 836.5           | 836.5             | 836.5            | 836.5             | 836.5             | 836.5            | 836.5            | 831               | 496             |
| Result<br>No.              | 1                | 8                | m                 | 4                 | ß                | 9                | 7                 | 80               | o,               | 10              | 11                | 12                | 13              | 14              | 15               | 16              | 17              | 18              | 19              | 20                | 21               | 22                | 23                | 24               | 25               | 56                | 27              |

| Sequence 2, Appli Sequence 22, Appl Sequence 13, Appl Sequence 73, Appl Sequence 10, Appl Sequence 11, Appl Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli  | Sequence 23, Appl<br>Sequence 1, Appli |
|--|--|
| US-09-546-117-2<br>US-09-169-205D-22<br>US-08-118-270-73<br>US-08-118-270-73<br>PCT-US33-08528-73<br>US-09-875-076-30<br>US-09-731-030A-11<br>US-09-731-030A-13<br>US-09-518-383-4<br>US-09-518-383-4<br>US-09-518-383-4<br>US-09-169-205D-20<br>US-09-169-205D-20<br>US-09-718-938-2<br>US-09-718-938-2<br>US-09-718-930A-15<br>US-09-711-938-2 | US-09-169-205D-23<br>US-09-274-752D-1  |
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| 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2  | 44.4                                   |

## ALIGNMENTS

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US-09-382-2004

US-09-382-2004

Patent No. 6482609

GENERAL INPORMATION:

APPLICANT: Munroe, Donald G.

APPLICANT: Munroe, Donald G.

APPLICANT: Momboj, Rajender

APPLICANT: Wooshesh, Fatemeh

APPLICANT: Vosa, Tejal B.

TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RF-

TITLE OF INVENTION: 108074-00002

CURRENT APPLICATION NUMBER: US/09/582,200A

CURRENT APPLICATION NUMBER: 09/22,995

PRIOR FILING DATE: 1998-12-30

PRIOR FILING DATE: 1998-12-30

PRIOR FILING DATE: 1998-04-03

PRIOR FILING DATE: 1998-04-03

PRIOR FILING DATE: 1998-04-03

PRIOR FILING DATE: 1998-12-30

PRIOR FILING DATE: 1998-14-03

PRIOR FILING DATE: 1998-12-30

NUMBER OF SEQ ID NOS: 14
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Best Local Similarity 100.
Matches 353; Conservative
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CORGANISM: Homo sapiens
US-09-582-200A-4
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Sequence 12, Application US/09582200A; Sequence 12, Application US/09582200A; Sequence 12, Application US/09582200A; Sequence 12, Application US/09582200A; GENERAL INFORMATION:
APPLICANT: Kamboj, Rajender
APPLICANT: Kaoshesh, Fateumeh
APPLICANT: Kooshesh, Fateumeh
APPLICANT: Gupta, Ashwani
TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE;
TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE;
FILE REFERENCE: 108074-00002
CURRENT PILING DATE: 1908-12-30
FRIOR FILING DATE: 1998-12-30
FRIOR FILING DATE: 1998-11-25
FRIOR FILING DATE: 1998-11-25
FRIOR FILING DATE: 1998-11-25
FRIOR FILING DATE: 1998-11-25
FRIOR FILING DATE: 1998-13-30
FRIOR FILING DATE: 1998-13-30
FRIOR FILING DATE: 1998-31-2-30
FRIOR SEQIENCE: PATENTION NUMBER: 60/070,185
FRIOR FILING DATE: 1998-31-2-30
FRIOR FILING DATE: 1998-31-3-30
FRIOR FILING DATE
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Sequence 19, Application US/09731030A

Patent No. 6566096

GENERAL INCORMATION:
APPLICANT: MUNROE, Donald G

APPLICANT: GUPTA, ABIWANI K.
TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
FILE REFERENCE: 8074-0015
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APPLICANT: Munroe, Donald G.
APPLICANT: Kambol, Rajender
APPLICANT: Kambol, Rajender
APPLICANT: Kambol, Rajender
APPLICANT: Kambol, Rajender
APPLICANT: Peters, Diana
APPLICANT: Peters, Diana
APPLICANT: Peters, Diana
APPLICANT: Hejal B.
APPLICANT: Wyas, Tejal B.
TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
FILE REFERENCE: 108074-00002
CURRENT APPLICATION NUMBER: UG/09/582,200A
CURRENT FILING DATE: 1998-12-30
FRIOR APPLICATION NUMBER: PCT/CA98/01195
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-11-25
PRIOR FILING DATE: 1998-11-25
PRIOR FILING DATE: 1998-10-000
PRIOR FILING DATE: 1998-11-25
PRIOR FILING DATE: 1998-10-03
NUMBER: 60/090,185
PRIOR FILING DATE: 1997-12-30
NUMBER: 60/090,185
PRIOR FILING DATE: 1997-12-30
NUMBER: PATER PAT
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Patent No. 6482609
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; ORGANISM: Homo sapiens
US-09-582-200A-6
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JUNEARAL INFUGARATION:

JUNDARAL INFUGARATION:

APPLICANT: Wantoe, Donald G.

APPLICANT: Ramboj, Rajender

APPLICANT: Referse, Diana
APPLICANT: Wooshesh, Fatemeh

APPLICANT: Vyas, Tejal B.

APPLICANT: Wooshesh, Retemeh

APPLICANT: Wooshesh, Resemen

TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY R

FILE REFERENCE: 108074-00002

CURRENT FILING DATE: 1998-12-30

PRIOR PILING DATE: 1998-12-30

PRIOR PELING DATE: 1998-12-30

PRIOR PELING DATE: 1998-12-30

PRIOR PELING DATE: 1998-12-50

PRIOR PELING DATE: 1998-04-03

PRIOR PILING DATE: 1998-04-03

PRIOR PILING DATE: 1999-12-30

PRIOR PILING DATE: 1999-11-25

PRIOR PILING DATE: 1999-11-25

PRIOR PILING DATE: 1999-11-25

PRIOR PILING DATE: 1999-11-25

PRIOR PILING DATE: 1997-12-30

PRIOR PILING DATE: 1997-12-30

PRIOR PILING DATE: 1997-12-30

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PRIOR PILING DATE: 1997-12-30
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                           FEATURE:
NAMEXKEY: misc feature
LOCATION: (273)..(273)
COTHER INPORMATION: Unknown Xaa refers to any amino acid
US-09-582-200A-2
                                                                                                                                                                      99.7%; Score 1803; DB 2;
99.4%; Pred. No. 2.8e-145;
iive 1; Mismatches 1;
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LOCATION: (272)..(274)
OTHER INFORMATION: Unknown Xaa
FEATURE:
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Best Local Similarity 99.4*
Matches 351; Conservative
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       ORGANISM: Homo sapiens
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SEQ ID NO 5
LENGTH: 353
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APPLICANT: Munrol, Rajender
APPLICANT: Ramboj, Rajender
APPLICANT: Kamboj, Rajender
APPLICANT: Kooblesh, Fatemeh
APPLICANT: Vyas, Tejal B.
APPLICANTON NUMBER: US/09/582,200A
CURRENT APPLICATION NUMBER: 09/22,995
PRIOR PILING DATE: 1998-12-30
PRIOR PLING DATE: 1998-12-30
PRIOR PLING DATE: 1998-04-03
PRIOR PLING DATE: 1998-04-03
PRIOR PLING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 14
SOFTHARE: Patentin version 3.1
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US-09-731-030A-19
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100.0%; Score 1809; DB 2;
Best Local Similarity 100.0%; Pred. No. 8.7e-146;
Matches 353; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/731,030A;
CURRENT FILING DATE: 1998-12-29;
PRIOR APPLICATION NUMBER: 60/070,184
FILING DATE: 1997-12-30;
NUMBER OF SEQ ID NOS: 21;
SOFTWARE: PatentIN Ver. 2.0;
SEQ ID NO 19;
TYPE: PRT
CREATE: PRT
CREATE: ORGANISM: UNKNOWN
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LENGTH: 353
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; Sequence 3, Application US/09274752D
; Patent No. 6812335
; GENERAL INFORMATION:
; APPLICANT: An Songahu
; TITLE OF INVENTION: Human Polypeptide Receptors for Lysophospholipids and
; TITLE OF INVENTION: Sphingolipids and Nucleic Acids Encoding the Same
; FILE REFERENCE: A-57501/DJSTAL
; CURRENT APPLICATION NUMBER: US/09/274,752D
; CURRENT FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 3
; SEQ ID NO 3
; LENGTH: 353
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ilarity 98.0%; Pred. No. 1.3e-141;
Conservative 1; Mismatches 6;
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US-09-274-752D-3
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Best Local
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Facent No. 648260
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Munroe, Donald G.
APPLICANT: Remboj, Rajender
APPLICANT: Potes Distance
APPLICANT: Potes Distance
APPLICANT: Vyas, Tejal B.
APPLICANT: Ocoshesh, Fatemeh
APPLICANT: Ocoshesh, Ratemeh
APPLICANT: Vyas, Tejal B.
APPLICANT: Wyas, Tejal B.
FILE REFERENCE: 106074-00002
CURRENT APPLICATION NUMBER: 05/22,995
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 60/109,885
PRIOR APPLICATION NUMBER: 60/109,885
PRIOR PILING DATE: 1998-04-03
PRIOR APPLICATION WUMBER: 60/000,610
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1999-11-25
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: PACHLIN VARIER: 60/000,610
PRIOR FILING DATE: PACHLIN VARIER: 60/000,610
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                                                                                                  Score 1803; DB 2;
Pred. No. 2.8e-145;
1; Mismatches 1;
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99.4%; Pred. No. 2.8e-145;
iive 1; Mismatches 1;
i LOCATION: (273)..(273)

j OTHER INFORMATION: Unknown Xaa = Leu or Pro
US-09-582-200A-5
                                                                                                                                                 1; Mismatches
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ORGANISM: human EDG-4 polypeptide
                                                                                               Query Match
Best Local Similarity 99.4%;
Matches 351; Conservative
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Best Local Similarity 99.4
Matches 351; Conservative
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US-09-582-200A-10
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                            JOSTANDA STATE OF TABLICATION US/08196989B

Patent No. 5585476

GENERAL INFORMATION:

APPLICANT: MACLEMENA, A. John

TITLE OF INVENTION: Molecular Cloning and Expression of

TITLE OF INVENTION: G-Protein Coupled Receptors

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville
STATE: FL

COUNTRY: US

STATE: FL

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopsy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURSSIFILING DATE: 15-FEB-1994

FILING DATE: 15-FEB-1994

STICHARLING SYSTEM FORMATHER.

APPLICATION NUMBER: US/08/196,989B
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89.9%; Score 1625.5; DB 1.

Best Local Similarity 89.5%; Pred. No. 3.3e-130;

Matches 316; Conservative 14; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
ATORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFRENCE/DOCKET NUMBER: MAC-100
TELEPOMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPAX: 904-372-5800
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TYPE: amino acid
STRANDEDNESS: single
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RESULT 9
US-08-196-989B-2
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89.5%; Pred. No. 3.3e-130;
tive 14; Mismatches 22; Indels
                                            GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
TITLE OF INVENTION: Molecular Cloning and Expression of
TITLE OF INVENTION: G-Frotein Coupled Receptors
NUMBER OF SEQUENCES: 14
CORRESPENDENCE ADDRESS:
ADDRESSE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,936
FILING DATE: December 6, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MAC-100C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-09-582-200A-11
; Sequence 11, Application US/09582200A
; Patent No. 6482609
Sequence 2, Application US/08760936 Patent No. 5856443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 352-375-8100
TELEPACH 352-375-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 89.5%
Matches 316; Conservative
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COUNTRY:
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61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
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Sequence 2, Application US/09225024

Patent No. 6518414

Patent No. 6518416

PAPLICANT: MacLennan, A. John

TITLE OF INVENTION: Molecular Cloning and Expression of TITLE OF INVENTION: Protein Coupled Receptors

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           IndelB
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,024
FILING DATE: 04-7AN-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/760,936
FILING DATE: 0-DEC-1996
FILING DATE: 15-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                        Query Match 89.9%; Score 1625.5; DB 2
Best Local Similarity 89.5%; Pred. No. 3.3e-130;
Matches 316; Conservative 14; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Sulte A-1
CITY: CITY: FL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 352-372-5800
; SEQ ID NO 24
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Rattus SP.
US-09-169-205D-24
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                                                                                APPLICANT: Peters, Diana
APPLICANT: Peters, Diana
APPLICANT: Kooshesh, Fatemeh
APPLICANT: Vyas, Tejal B.
APPLICANT: Gupta, Ashwani
ITLEOP OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
FILE REPERENCE: 108074-00002
CURRENT APPLICATION NUMBER: US/09/582,200A
CURRENT APPLICATION NUMBER: US/022,995
PRIOR APPLICATION NUMBER: PO/222,995
PRIOR APPLICATION NUMBER: 60/109,885
PRIOR FILING DATE: 1998-11-25
PRIOR FILING DATE: 1998-11-25
PRIOR PELING DATE: 1998-04-03
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1998-11-25
PRIOR PELING DATE: 1998-11-25
PRIOR FILING DATE: 1998-11-36
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 352
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Patent No. 648592
GENERAL INFORMATION:
APPLICANT: Erikson, James
APPLICANT: Kiefer, Michael
APPLICANT: Kiefer, Michael
APPLICANT: Kiefer, Michael
TITLE OF INVENTION: METHODS FOR DETECTING COMPOUNDS WHICH MODULATE THE
TITLE OF INVENTION: ACTIVITY OF AN LPA RECEPTOR
FILE REFERENCE: 252/004
CURRENT APPLICATION NUMBER: US/09/169,205D
CURRENT FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: rat EDG-4 polypeptide
US-09-582-200A-11
                        APPLICANT: Munroe, Donald G.
APPLICANT: Kamboj, Rajender
APPLICANT: Peters, Diana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-169-205D-24
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74 KKFHRPMYYFIGNLALSDLLAGVAYTANLLLSGATTYKLTPAQWFLREGSMFVALSASVF 133
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                                                                                                                              SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVF
Gaps
12;
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84; Indels
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GENERAL INFORMATION:

APPLICANT: MacLennan, A. John

TITLE OF INVENTION: Molecular Cloning and Expression of

TITLE OF INVENTION: G-Protein Coupled Receptors

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,989B
FILING DATE: 15-FEB-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MAC-100
TELECOMMULICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
Mismatches
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Patent No. 5585476
60;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
159; Conservative
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US-08-196-989B-4
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CURRENT APPLICATION NUMBER: US/09/262,477A

EARLIER FILING DATE: 1999-03-04

EARLIER FILING DATE: 1999-03-09

EARLIER FILING DATE: 1998-03-09

EARLIER FILING DATE: 1998-03-09

EARLIER FILING DATE: 1998-03-09

EARLIER FILING DATE: 1998-05-28

NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 VFIICWLPAFSILLLDSTCPVRACPVLYKAHYPFAFATLNSLLNPVIYTWRSRDLRREVL 300
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                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                           Query Match 89.9%; Score 1625.5; DB 2; Best Local Similarity 89.5%; Pred. No. 3.3e-130; Matches 316; Conservative 14; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09262477A Patent No. 6423508 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: George Livi
APPLICANT: Derk Berggma
APPLICANT: Jeffrey Stadel
APPLICANT: Winnie Chan
APPLICANT: Randall Johnson
APPLICANT: Shelagh Wilson
APPLICANT: On Chambers
APPLICANT: Phillipe Robert
APPLICANT: Nassirah Khandoudi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.9%;
                                               352 amino acids
  INFORMATION FOR SEQ ID NO:
                      SEQUENCE CHARACTERISTICS
                                                                                       single
                                                                                                                              MOLECULE TYPE: peptide
                                             LENGTH: 352 amino
TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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231 LLKTVTIVLGVFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTW 290
                                                              15 SQVSDYGNYDIIVRHYNYTGKLNIGVEKDHGIKLTSVVFILLCCLIILENIFVLLTIWKT 74
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Search completed: December 4, 2005, 06:24:24 Job time: 34.5 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, A
Sequence 26,
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                                                                                                                             US-10-084-507B-22
1809
1 MGSLYSEYLNPNKVQEHYNY ......LERGMHMPTSPTFLEGNTVV 353
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Sequence 6,
Sequence 2,
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-10-851-667A-26
US-10-992-577-2
US-10-992-577-6
US-10-992-577-6
US-10-992-577-6
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US-10-980-388-112
US-10-980-388-112
US-10-980-388-112
US-10-980-388-117
                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                        26661 segs, 4788334 residues
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Maximum Match 100%
Listing first 45 summaries
                                                  - protein search, using sw model
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| 26 105.5 5.8 323 6 US-10-980-388-119 Sequence 27 103.5 5.7 181 6 US-10-980-388-110 Sequence 28 100 5.5 337 6 US-10-980-388-115 Sequence 29 27 20.4 6 US-10-980-388-115 Sequence 30 92.5 5.1 286 6 US-10-980-388-8 Sequence 31 92.5 5.1 286 6 US-10-980-388-8 Sequence 32 89.5 4.9 628 7 US-11-092-389-402 Sequence 33 86.5 4.8 313 6 US-10-980-388-96 Sequence 34 86.5 4.8 313 6 US-10-980-388-96 Sequence 36 86.5 4.8 337 6 US-10-980-388-96 Sequence 37 86.5 4.8 431 6 US-10-980-388-96 Sequence 38 86 4.8 337 6 US-10-980-388-96 Sequence 39 86.5 4.8 47 394 6 US-10-980-389-16 Sequence 39 86.5 4.8 47 394 6 US-10-980-389-17 Sequence 39 86.5 4.8 337 6 US-10-980-389-16 Sequence 39 86.5 4.8 337 6 US-10-980-389-16 Sequence 39 86.5 4.8 337 6 US-10-980-389-18 Sequence 39 86.5 4.6 205 7 US-11-082-389-378 Sequence 39 86.5 4.6 508 6 US-10-980-389-378 Sequence 39 86.5 4.6 508 6 US-10-88-389-378 Sequence 39 86.5 4.5 508 6 US-10-88-389-378 Sequence 30 86.5 4.5 508 6 US-10-88-389-378 Sequence 43 80.5 4.5 508 6 US-10-88-389-378 Sequence 44 82.5 4.5 508 6 US-10-88-389-378 Sequence 44 82.5 4.6 508 6 US-10-88-389-378 Sequence 44 82.5 4.5 508 6 US-10-88-389-378 Sequence 44 82.5 4.5 508 6 US-10-88-389-34 Sequence 44 82.5 508 6 US-10-88-389-34 Sequence 44 82.5 4.5 508 6 US-10-88   | 119, App          | 100, App          | 115, App          | 68, Appl         | 199, App          | 3, Appli        | •                 | 950, App          | 33, Appl         | 96, Appl         | 116, App          | 3566, Ap           |                   | 52, Appl          | 374, App          | 378, App          | 201, App          | 3306, Ap           | 7826, Ap     | 412, App |
|--|-------------------|-------------------|-------------------|------------------|-------------------|-----------------|-------------------|-------------------|------------------|------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------|----------|
| 5.5 5.7 5.8 5.7 5.8 5.7 5.9 5.7 5.9 5.9 5.9 5.9 5.9 5.9 5.9 5.9 5.9 5.9  | Sequence :        | Sequence          | Sequence          |                  | Sequence          |                 |                   |                   | Sequence         |                  |                   |                    |                   |                   | Sequence          | Sequence          | Sequence          | Sequence           | •            |          |
| 5.5 5.7 5.8 5.7 5.8 5.7 5.9 5.7 5.9 5.9 5.9 5.9 5.9 5.9 5.9 5.9 5.9 5.9  | US-10-980-388-119 | US-10-980-388-100 | US-10-980-388-115 | US-10-980-388-68 | US-10-858-730-199 | US-11-099-691-8 | US-11-082-389-402 | US-10-467-657-950 | US-10-980-388-63 | US-10-980-388-96 | US-10-980-388-116 | US-10-793-626-2566 | US-10-793-626-444 | US-10-392-234A-52 | US-11-082-389-374 | US-11-082-389-378 | US-10-858-730-201 | US-10-793-626-3306 | 10-467-657-7 |          |
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| 26 105.5<br>27 103.5<br>29 92.5<br>30 92.5<br>31 92.5<br>32 92.5<br>33 88.5<br>34 87.5<br>36.5<br>37 86.5<br>38 86.5<br>38 86.5<br>40.8<br>39 86.5<br>40.8<br>30 86.5<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8<br>40.8 | 323               | 181               | 337               | 204              | 286               | 336             | 628               | 486               | 313              | 358              | 389               | 431                | 337               | 394               | 202               | 202               | 301               | 392                | 208          | 462      |
| 26 105.5<br>27 103.5<br>29 29 29 31 32 31 32 33 33 4 87.5<br>36.5 36.5 36.5 36.5 36.5 36.5 36.5 36.5   | 5.8               | 5.7               | 5.5               | 5.4              | 5.1               | 5.1             | 4.9               | 4.9               | 4.8              | 4.8              | 4.8               | 4.8                | 4.8               | 4.7               | 4.6               | 4.6               | 4.6               | 4.6                | 4.6          | 4.5      |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0  | 105.5             | 103.5             | 100               | 97               | 92.5              | 92              | 89.5              | 88                | 87.5             | 86.5             | 86.5              | 86.5               | 98                | 84.5              | 83.5              | 83.5              | 83.5              | 83                 | 82.5         | 82       |
|  | 26                | 27                | 28                | 53               | 30                | 31              | 32                | 33                | 34               | 35               | 36                | 37                 | 38                | 39                | 40                | 41                | 42                | 43                 | 44           | 45       |

## ALIGNMENTS

```
STATEMENT MILLEY, Duane D.

APPLICANT: MILLEY, Gabor
APPLICANT: Tigyl, Gabor
APPLICANT: Dalton, James T.
APPLICANT: Datton, James T.
APPLICANT: Bardar, Vineet M.
APPLICANT: Sardar, Vineet M.
APPLICANT: Brod, Don B.
APPLICANT: Wang, Dean
APPLICANT: Mang, Dean
APPLICANT: Histon, Karoly
APPLICANT: Fischer, David J.
APPLICANT: Vineg, Tamas
APPLICANT: Vineg, Vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTI 197
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                        Sequence 2, Application US/11067884 Publication No. US20050261252A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::
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Best Local Similarity 34.61
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Homo sapiens
US-11-067-884-2
US-11-067-884-2
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Sequence Sequence Sequence

Sequence Sequence Sequence

US-11-068-686-4 US-10-502-145-1 US-10-131-826A-18

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63 KFHSAMYLFIGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVFS 122
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APPLICANT: Fischer, David J.
APPLICANT: Virag, Tamas
APPLICANT: Virag, Tamas
APPLICANT: Virag, Tamas
APPLICANT: Wisser, Namas
APPLICANT: Nusser, Namas
TITLE OF INVENTION: USE
FILE REPRENCE: 20609/307
FILE REPRENCE: 2005-02-28
FRICK APPLICATION NUMBER: 60/190,370
FRICK APPLICATION NUMBER: 60/190,370
FRICK APPLICATION NUMBER: 09/811,838
FRICK APPLICATION NUMBER: 09/811,838
FRICK APPLICANION NUMBER: 09/811,838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 353;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.6%; Score 481.5; DB 7;
llarity 32.2%; Pred. No. 5.3e-34;
Conservative 73; Mismatches 121;
                                           315 LROSTRESVHYTSSAQGGASTRIMLP 340
  306 ----WRPGVGVQGRRRGGTPGHHLLP 327
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US-10-851-667A-26
S-10-851-667A-26
S-20-26 Application US/10851667A
Publication No. US20050260608A1
GENERAL INFORMATION:
                                                                                                                                                             Sequence 6, Application US/11067884
Publication No. US20050261252A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 RDLRREVLRPLQCW 306
                                                                                                                                                                                                                                                                                                                           Elrod, Don B.
Xu, Huiping
Baker, Daniel L.
Wang, Dean
                                                                                                                                                                                                                                                        Tigyi, Gabor
Dalton, James T.
Sardar, Vineet M.
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SEQ ID NO 6
LENGTH: 353
                                                                                                                                                                                                                                APPLICANT: Miller, Duane D. APPLICANT: Tigyi, Gabor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 101; Conserv
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APPLICANT:
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                                           198 FSIILLAV-VALYVRIYCVVR-----SSHADMAAPQ----TLALLKTVTIVLGVFIVC 245
                                                                                                                                     246 WLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVLRPLQC 305
                                                                                                                                                                  271 WTPGLVLLLDVCCP--QCDVLAYEKFFLLLAEFNSAMNPIIXSYRDKEMSATFRQILCC 328
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                                                                                        213 FNLVTFVVMVVLYAHIFGYVRORTMRMSRHS--SGPRRNRDTMMSLLKTVVIVLGAFIIC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVFSLLAIAIBRHVAIAKV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLLVFLLMVAVYTRIFFYVRRRVQRMAEHVSCHPRYRETTLSLVKTVVIILGAFVVCWTP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 AFSILLLD-YACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVLRPLOC-- 305
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APPLICANT: Fischer, David J.
APPLICANT: Fischer, David J.
APPLICANT: Virag, Tama
APPLICANT: Nusser, Nora
APPLICANT: Nusser, Nora
TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF TITLE OF INVENTION: USB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 YNYTKETLETQETTSROVASAFIVILCCAIVVENLLVLIAVARNSKFHSAMYLFLGNLAA
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                                                                                                                                                                                                                              306 WRPGVGCRRRGGTPGHHLLPLRSSSSLER----GMH 339
                                                                                                                                                                                                                                                                           QR----SENPTGPTESSD----RSASSLNHTILAGVH 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/11/067,884
CURRENT FILING DATE: 2005-02-28
PRIOR APPLICATION NUMBER: 60/190,370
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/11067884 Publication No. US20050261252A1 GENERAL INFORMATION:
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Baker, Daniel L.
Wang, Dean
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APPLICANT: Tigyi, Gabor
APPLICANT: Dalton, James T.
APPLICANT: Sardar, Vineet M.
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US-11-067-884-4
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APPLICANT:
APPLICANT:
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APPLICANT Gerald, Christophe P.G.
APPLICANT Gerald, Christophe P.G.
APPLICANT Gerald, Christophe P.G.
APPLICANT Gerald, Christophe P.G.
APPLICANT Bonows, Kenneth A.
APPLICANT BOTOWSKY, Beth E.
APPLICANT BOTOWSKY, Beth E.
TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
TITLE OF INVENTION: And Uses Thereof
FILE REFERENCE: 57155-D/5PW
CURRENT APPLICATION NUMBER: US/09/538,036
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-09-24
PRIOR PRILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: 09/161,113
PRIOR APPLICATION NUMBER: 09/161,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 SRRRARVVHMLVMVALFFTLSWLPLWALLLLIDYGQLSAPQLHLVTVYARPF---AHWL- 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 VAYALIFLIC---MYGNTLYCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDN 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 SVTLRLTPVQWFAREGSAF------ITLSASVFSLLAIAIER-----HVAIAK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 VKLYGSDKSCRMLLLIGASWLISLVL---GGLPILGWNCLGH--LEACSTVLPLYAKHYV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 LC------SSHADMAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 -CWEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMYARIARKLCQAPGPAPGGEEAADPRA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 PQTLALLKTVTIVLGVFI-VCWLPAFSILLL-DYA------CPVHSCPILYKAHYLF 274
                                                                                                                                                                                                                                                                                                                                                                             35 VASAFIVILCCAIVVENLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSG
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376 VRPSDSGLPSESGPSSGAPRPGRLPLRNGRVAHHGLPREGPGCSHLPLTIPAW 428
                                                                                                                                                                                                                                                                                                                             Indels 133;
                                                                                                                                                                                                                                                                                Length 430;
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                                                                                                                                                                                                                                                                              12.5%; Score 226.5; DB 6; 24.7%; Pred. No. 1.8e-12; arrive 58; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 AVSTLNSLLNPVIYTWRSRDLRR---EVLRPLOCWRP-
                  PRIOR APPLICATION NUMBER: 09/161,113
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10992577 Publication No. US20050260687A1 GENERAL INFORMATION:
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US-10-992-577-2
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 24.74
Matches 102; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 432
                                                                                                                                                                            TYPE: PRT
CORGANISM: Homo sapiens
US-10-992-577-8
                                                                                                                                                    LENGTH: 430
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APPLICANT: Shohami, Esther

TITLE OF INVENTION: METHODS, KITS AND PHARMACEUTICAL COMPOSITIONS FOR DIAGNOSING,
TITLE OF INVENTION: DELAYING ONSET OF, PREVENTING AND/OR TREATING OSTEOPOROSIS
FILE REFERENCE: 28030
CURRENT APPLICATION NUMBER: US/10/851,667A
CURRENT FILING DATE: 2004-05-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.2
SEQ ID NO 26
LENGTH: 360
LENGTH: 360
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Publication No. US20050260687A1

GENERAL INFORMATION:

APPLICANT: Gerald, Christophe P.G.

APPLICANT: Borowsky, Beth B.

APPLICANT: Craig, Douglas A.

APPLICANT: Craig, Douglas A.

TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors

TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors

TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors

TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors

TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors

TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors

FILE REPERENCE: 57155-D/JFW

CURRENT APPLICATION NUMBER: US/10/992,577

CURRENT APPLICATION NUMBER: 09/405,558

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-09-24

PRIOR FILING DATE: 1999-02-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 GMARWRLDVRLAKTYGLVLAVLJICWFPVLALMAHSLATTLSD---QVKKAFAFCSMLCL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 HSAMYLFLGNLAASDLLAGVAF-----VANTLLSGSVTLRLTPVQWFAREGSAFITL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 RKPSYLFIGSLAGADFLASVVFACSFVNFHVFHGVDSKAVFL-----LKIGSVIMTF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 SASVFSLLAIAIERHVAIAKVKLYGSDKSC----RMLLLIGASWLISLVLGGLPILGWWC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 LGHLEACSTVLPLYAKHYVLCVVTIFSIILLAVVALYVRI-----YCVVRSSHADMAAP 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 VTEIANGSKDGLDSNPMKDYMILSGPQKTAVAVLCTLLGLLSALENVAVLYLILSSHXLR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 VQEHYNYTKETLETQETTSRQVAS----AFIVILCCAI----VVENLLVL-IAVARNSKF 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.7%; Score 284; DB 6; Length 360;
25.9%; Pred. No. 2.2e-17;
tive 65; Mismatches 133; Indels
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| LOCATION: (63)...(63)

| CTHER INFORMATION: Non-synonymous polymorphism: Gln or Arg

US-10-851-667A-26
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290 INSMVNPVIYALRSGEIRSSAHHCLAHWKKCVRGLGSEAK 329
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Matches 88; Conservative
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10 NPNKVQEH-----YNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARNSK
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-510-018-2
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US-LID-924-2).-6

Sequence 6, Application US/10992577

Publication No. US20050260687A1

Sequence 6, Application No. US20050260687A1

APPLICANT: Borneth A.

APPLICANT: Jones, Kenneth A.

APPLICANT: Borowsky, Beth E.

APPLICANT: Craig, Douglas A.

APPLICANT: Craig, Douglas A.

TITLE OF INVENTION: And Uses Thereof

FILE REFERENCE: 57155-D/JPW

CURRENT APPLICANTON NUMBER: US/09/538,036

FRIOR FILING DATE: 2004-11-18

PRIOR PRILNG DATE: 1999-09-24

PRIOR FILING DATE: 1999-09-24

PRIOR FILING DATE: 1999-09-25

PRIOR FILING DATE: 1999-02-25

PRIOR FILING DATE: 1999-02-25

PRIOR FILING DATE: 1998-09-25

PRIOR PRING APPLICATION NUMBER: 09/161,113

PRING APPLICATION OF 0
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                                                               19;
                                                                                                                                                                                                                       SDLLVGIPCMPTTLVDNLIT------GWPFDNATCKMSGLVQGMSVSASVFTLV 135
                                                                                                                                                                                                                                                                       AIAIER-----HVAIAKVKLYGSDKSCRMLLLLIGASWLISLVL---GGLPILGWNCLGH- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARDTEEAVAEGGRISRRRARVVHMLVMVAL---FFTLSWLPLWVLLLLIDYGELSELQLH 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 LLSVYAFPL---AHWL---AFFHSSANPIIYGYFNENFRRGFQAAFRAQLCWPPWAAHKQ 360
                                                                                                                                                                                    78 SDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAF------ITLSASVFSLL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 -CPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRR---EVLRPLQCWRP---- 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GVGVQGRRRGGTPGHHLLPLRSSSSLERG----- 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 AYSERPNRLLRRRVVVDVQPSDSGLPSESGPSSGVPGPGRLPLRNGRVAHQDGPGEGPGC 420
                                                                                                                            28 ISLIFSSYYQHSSYVAAMFIAAYVLIFLLCMVGNTLVCFIVLKNRHMRTVTNMFILNLAV 87
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                      TKETLETQETTSRQVASAFI ---VILCCAIVVENLLVLIAVARNSKFHSAMYLFLGNLAA
                                                                                                                                                                                                                                                                                                                                                      176 -LEACSTVLPLYA-----KHYVLCVVT-IFSIILLAVVALYVRI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                      213 ----YCVVRSSHADMAAPQTLALLKTVTIVLGVFIVCWLPAFSILLL-DYA-----
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                 Query Match
11.9%; Score 215.5; DB 6; Length 432;
Best Local Similarity 23.7%; Pred. No. 1.6e-11;
Matches 102; Conservative 57; Mismatches 140; Indels 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95;
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                   Query Match
Best Local Similarity
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Sequence 2, Application US/10510018
Publication No. US20050244896A1
Fublication No. US20050244896A1
FUBLICANT: Golz, Stefan
APPLICANT: Bruggemeier, Ulf
APPLICANT: Bruggemeier, Ulf
TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
TITLE OF INVENTION: Neuropeptide FF Receptor 2 (NPFF2)
FILE REFERENCE: Le A 35 945
CURRENT APPLICATION NUMBER: CT/FE2003/002962
FRIOR APPLICATION NUMBER: PCT/FE2003/002962
FRIOR PILING DATE: 2003-03-21
FRIOR FILING DATE: 2003-03-21
FRIOR FILING DATE: 2003-04-10-01
FRIOR FILING DATE: 2003-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
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                                                                                                                      64 FHSAMYLFLGNLAASDLLAGVAFVANTLLS------GSVTLRLTFVQWFAREGSAFIT 115
                                                                                                                                                                                                                                      116 LSASVFSLLAIAIERHVAIA---KVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNC 172
                                                                                                                                                                                                                                                                        206 VALYVRIYCVVRSSHADMAAPQT-----LALLKTVTIVLGVFIVCWLPAF 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 LSASVFSILALALALERHVAIA---KVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNC 172
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63
                                     18 NVNDTKHLYSDINITYVNYYLHQPQVAAIFIISYFLIFFLC--MMGNTVVCFIVMRNKH
                                                                                                                                                           ----LCVVTIFSIILLAV
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231 VAASVFILVALAVDRRQCVVYPFKPKL--TIKTAFVIIMI--IWVLAITI------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 SILLL-DYA-----CPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRR 297
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RESULT 11
US-10-980-388-118
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                                                                                                                                                                                                                                                                                                                                               LENGTH: 440
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                                                                                                                                                                                                               APPLICANT: Jones, Kenneth A.

APPLICANT: Bonini, James A.

TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors

TITLE OF INVENTION: And Uses Thereof

FILE REFERENCE: 57155-D/JFW

CURRENT APPLICATION NUMBER: US/09/538,036

PRIOR FILING DATE: 1999-09-24

PRIOR FILING DATE: 1999-09-24

PRIOR FILING DATE: 1999-02-22

PRIOR FILING DATE: 1999-02-22

PRIOR FILING DATE: 1999-02-22

PRIOR FILING DATE: 1999-02-25

NUMBER OF SEQ ID NOS: 71

SOOTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 LLAGVAFVANTLLS------GSVTLRLTPVQWFAREGSAFITLSASVFSLLAIAIERH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLVGIFCMPITLLDNIIAGWPFGSSMCKISGLV----QG---ISVAASVFTLVAIAVDRF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----REVLRPLQCWRPG 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----HADMAAPQTLALLKTVTIVLGVFIVCWLPAFSILLL-DYA-----C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 YTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARNSKFHSAMYLFLGNLAASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GWNCLGHLEACSTVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSS-----
  297
                     394 TLMMLSDYADLSPNELQIINIXIYPFAHWL---AFGNSSVNPIIYGFFNENFRR 444
251 SILLL-DYA-----CPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 VAIA---KVKLYGSDKSCRMLLLIGASWLISLVLGGLPIL-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.2%; Score 202.5; DB 6;
ilarity 22.6%; Pred. No. 1.9e-10;
Conservative 73; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 VGVQGRRRGGTPGHHLLPLRSSSSLERGMHMPTS 343
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                                                                                                                                       Sequence 44, Application US/10992577
Publication No. US/005060687A1
GENERAL INFORMATION:
APPLICANT: Gerald, Christophe P.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-10-502-893-2
; Sequence 2, Application US/10502893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 89; Conserv
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APPLICANT: Vogell, Gabriel
APPLICANT: Parodi, Luis A.
APPLICANT: Parodi, Luis A.
APPLICANT: Hiebsch, Ronald R.
APPLICANT: Lind, Peter
APPLICANT: Kaytes, Paul S.
APPLICANT: Ruff, Valerie
APPLICANT: Ruff, Valerie
APPLICANT: Wood, Linda M.
APPLICANT: Wood, Linda M.
APPLICANT: Wood, Linda M.
APPLICANT: Wood, Linda S.
TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related App FILE REFERENCE: 0032-5.USI
CURRENT APPLICATION NUMBER: US/10/980,388
CURRENT FILING DATE: 2004-11-02
                                                                              APPLICANT: Golz, Stefan
APPLICANT: Buggemeier, Ulf
APPLICANT: Burggemeier, Ulf
APPLICANT: Geerts, Andreas
TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with a New
TITLE OF INVENTION: Human 5HT6 Receptor
FILE REFERENCE: LeA 35 827
CURRENT APPLICATION NUMBER: US/10/502,893
CURRENT FILING DATE: 2004-07-27
PRIOR PILING DATE: 2003-01-20
PRIOR PILING DATE: 2003-01-20
PRIOR PELING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 5
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4.7e-10;
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Publication No. US20050255490A1
GENERAL INFORMATION:
APPLICANT: Vogeli, Gabriel
                                                   APPLICANT: Bayer HealthCare AG APPLICANT: Golz, Stefan
US20050255529A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.2 SEQ ID NO 2
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US-10-502-893-2
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 ISLVLGGLP------ILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSIILLA 204
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APPLICANT: Fischer, David J.
APPLICANT: Virag, Tamas
APPLICANT: Nusaer, Nora
TITLE OF INVENTION: LDA
TITLE OF INVENTION: USE
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PRIOR PILING DATE: 2000-03-13
PRIOR PILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-11
PRIOR PLING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/219,492
PRIOR APPLICATION NUMBER: 60/218,492
PRIOR PILING DATE: 2000-07-20
PRIOR PLING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PATENTIN VERBION 3.0
LENGTH: 342
US/09/791,932
                                                                                                                      APPLICATION NUMBER: 60/184,304
FILING DATE: 2000-02-23
APPLICATION NUMBER: 60/184,303
FILING DATE: 2000-02-23
APPLICATION NUMBER: 60/184,397
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APPLICATION WINGHER: 60/184,247
FILING DATE: 2000-02-23
APPLICATION NUMBER: 60/188,880
                                FILING DATE: 2001-02-23
APPLICATION NUMBER: 60/184,305
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Publication No. US20050261252A1
GENERAL INFORMATION:
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                                                                                           FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-118
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US-11-067-884-8
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APPLICANT: Vogeli, Gabriel
APPLICANT: Parodi, Luis A.
APPLICANT: Hiebsch, Ronald R.
APPLICANT: Lind, Peter
APPLICANT: Raytes, Paul S.
APPLICANT: Ruff, Valerie
APPLICANT: Ruff, Valerie
APPLICANT: Wood, Linds S.
TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl CURRENT APPLICATION NUMBER: US/10/980,388
CURRENT APPLICATION NUMBER: US/10/980,388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 LALLKTVTIVLGVFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVST-----LNS
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FILE REFERENCE: 20609/305
CURRENT APPLICATION NUMBER: US/11/067,884
CURRENT FILING DATE: 2005-02-28
PRIOR PELIGATION NUMBER: 60/190,370
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 09/811,838
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 26
SOFWARE: PATENTIN VET: 2.1
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PRIOR APPLICATION NUMBER: US/09/791,932
PRIOR PILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/184,305
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,304
PRIOR PILING DATE: 2000-02-23
PRIOR PILING DATE: 2000-02-23
PRIOR PILING DATE: 2000-02-23
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Publication No. US20050255490A1
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Search completed: December 4, 2005, 06:42:27 Job time: 7 secs
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SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 934
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nes 64; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 SVTLRLTPVQWFAREG--SAFITLS----ASVFSLLAIAIERHVAIAKVKLYGSDKSCR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 M-LLLIGASWLISLVLGGLPILGWNCLGHLE---ACSTVLPLYAKHYVLCVVTIFSIILL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 VASAFIVILCCAIVVENLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSG 94
PRIOR APPLICATION NUMBER: 60/184,397
PRIOR PILING DATE: 2000-02-23
PRIOR PILING DATE: 2000-02-23
PRIOR PLING DATE: 2000-02-23
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 2000-02-31
PRIOR PLING DATE: 2000-03-13
PRIOR PLICATION NUMBER: 60/189,880
PRIOR PILING DATE: 2000-07-11
PRIOR PELICATION NUMBER: 60/217,370
PRIOR PELICATION NUMBER: 60/218,492
PRIOR PILING DATE: 2000-07-20
PRIOR PILING D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 LYSEYL------NPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPSQYLMELSEEHSWMSNQTDLHY----VLKPGEVAT---ASIFFGILWLFSIFGNSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
9.3%; Score 167.5; DB 6; Length 508;
Best Local Similarity 24.7%; Pred. No. 2e-07;
Matches 49; Conservative 48; Mismatches 84; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.9%; Score 143; DB 6; Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10627633

Publication No. US200502507201

GENERAL INFORMATION:
APPLICANT: Charles, Andrew David
APPLICANT: Brennand, John Charles
APPLICANT: Hart, Kevin Anthony
ITILE OF INVENTION: NOVel Compound
FILE REFERENCE: 1991-221
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: 09/722,342
PRIOR APPLICATION NUMBER: 09/722,342
PRIOR APPLICATION NUMBER: 60/172,146
PRIOR APPLICATION NUMBER: 60/172,146
PRIOR APPLICATION NUMBER: 60/172,146
PRIOR SEQ ID NOS: 6
SOFTWARE: PARENTIN VETSION 3.2
SEQ ID NO 2:
SEQ ID NO 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 VMIACYSVVFCAARROHA 224
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Best Local Similarity 24.2%
Matches 86; Conservative
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ORGANISM: Homo sapiens
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US-10-627-633-2
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51 NLLVLIAVARNSKFHSAMYLFLGNLAASDLL--AGVAFVANTLLSGSVTLRLTPVQW-FA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 REGSAFIT-----LSASVFSLLAIAIERHVAIAKV-----KLYGSDKSCRMLLLIGA 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 ALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLGVFIVCWLPAFSILLLDYACPVH--SC 264
                                                                                                                                                                                                                                                                                                194 FVTPVLFFYGSNWDSH---CNYFLPSSWEGTAYTVIHFLVGFVIPSVLILLFYQKVIKYI 250
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                                                                                                                      107 AREGSAFITLSASVFSLLAIAIERHVAIA----KVKLYGSDKSCRMLLLIGASWLI--S 159
                                                                                                                                                                                -----QYLTPGVQIYVLLSICIDRFYTIVYPLSFKVSREKAKK------MIAASWIFDAG 193
                                                                                                                                                                                                                                             160 LVLGGLPILGWNCLGHLEACSTVLP-----LYAKHYVLCVVTIFSIILL----AVVALY 209
                                                                                                                                                                                                                                                                                                                                                                    210 VRIYCVVRSSHADM-AAPQT-LALLKTVTIVLGVFIVCWLPAFSILLL-----DYACPV 261
                                                                                                                                                                                                                                                                                                                                                                                                       : : | : : | : : | : : | : : | : : | : : | 87 CLVIHRSRRIQSTINYFVVSMACADLLISVASIPFVLLQFTIGRWILGSAICKV--VRYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
FURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 HSCPILYKAHYLFA----VSTLNSLINPVIYTWRSRDLRREV-----LRPLQCWR 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 143; DB 6; Length 48; Pred. No. 2.2e-05; 57; Mismatches 121; Indels
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   LIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLLS--
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This Face Control (Uspin)

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241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300  
241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
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Sequence 17, Appl
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Sequence 22, Appl
                                                                                                                                         (without alignments)
1277.002 Million cell updates/sec
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Sequence 4,
Sequence 3,
Sequence 8,
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1 MGSLYSEYLNPNKVQEHYNY.......LERGMHMPTSPTFLEGNTVV 353
                                                                                                                    December 4, 2005, 06:23:06; Search time 115.5 Seconds
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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(cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-084-507B-17
US-09-842-16-8
US-09-917-228-9
US-09-904-099-33
US-10-228-567A-508
US-10-228-767-19
US-10-393-870-3
US-10-421-828-8
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US-10-421-828-8
US-10-421-828-8
US-09-771-063-4
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US-09-764-886-47
US-09-764-886-47
US-09-764-886-74
US-09-764-891-5338
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US-09-904-099-5
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US-10-633-438-65
US-10-901-772-65
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Patent No. US20020142375A1
GENERAL INFORMATION:
APPLICANT: MINROR, Donald G
APPLICANT: ASHWANI K.
TITLE OF INVENTION: MARMALIAN EDG-7 RECEPTOR HOMOLOGS
FILE REFERENCE: 8074-0015
CURRENT FILING DATE: 1998-12-29
PRIOR APPLICATION NUMBER: 60/070,184
PRIOR FILING DATE: 1997-12-30
NUMBER: OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.0
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100.0%; Pred. No. 3.4e-156;
ive 0; Mismatches 0;
US-11-026-435-8
US-09-971-228-13
US-09-861-455-2
US-09-861-455-2
US-09-169-4-09-1
US-10-98-192-786
US-10-25-567A-237
US-10-25-567A-237
US-10-25-567A-237
US-10-25-567A-237
US-10-25-567A-237
US-10-25-567A-237
US-10-25-567A-237
US-10-25-567A-237
US-10-25-567A-237
US-10-25-11-462-2
US-10-491-545A-30
US-10-491-545A-30
US-10-491-545A-30
US-10-491-545A-30
US-10-491-314-55760
US-09-971-228-15
US-10-08-971-228-15
US-09-96-711-2
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Matches 353; Conservative
  TYPE: PRT
ORGANISM: Unknown
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US-09-731-030A-19
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301 RPLQCWRPGVGVGCRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353
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| GENERAL INFORMATION:
| APPLICANT: KAMBOJ, RAJENDER
| APPLICANT: KAMBOJ, RAJENDER
| APPLICANT: PETERS, DIANA
| APPLICANT: PETERS, DIANA
| APPLICANT: VYAS, TEJAL B.
| APPLICANT: GUTTA, ASHWANI K.
| TILLE OF INVENTION: AN ISOLATED HUMAN EDG-4 RECEPTOR
| FILE REFERENCE: 108074-00023
| CURRENT APPLICATION NUMBER: US/10/084,507B
| CURRENT FILING DATE: 1998-12
| PRIOR FILING DATE: 1998-12-30
| PRIOR FILING DATE: 1998-11-25
| PRIOR APPLICATION NUMBER: 60/070,185
| PRIOR FILING DATE: 1998-14-03
| WUMBER OF SEQ ID NOS: 24
| SOFTWARE PATENTIN VEY: 2.1
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Best Local Similarity 100.0%; Pred. No. 3.4e-156;
Matches 353; Conservative 0; Mismatches 0;
                                                                                                 Sequence 22, Application US/10084507B
Publication No. US20030054452A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Derk J. Bergsma
APPLICANT: Nabil Elshourbagy
APPLICANT: Pamela Lane
APPLICANT: Xiaotong Li
APPLICANT: Jeffrey L. Mooney
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Jeffrey L. Mooney
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Sequence 17. Application US/10084507B

Publication No. US20030054452A1

GENERAL INFORMATION:

APPLICANT: MANROE, DANALD G.

APPLICANT: KAMBOJ, RAJENDER

APPLICANT: KOCSHESH, FATEMEH

APPLICANT: COCSHESH, FATEMEH

APPLICANT: WAS, TEJAL B.

APPLICANT: GUPTA, ASHWANI K.

ITLE OF INVUNITION AN ISOLATED HUMAN EDG-4 RECEPTOR

ITLE OF INVUNITION AN ISOLATED HUMAN EDG-4 RECEPTOR

FILE REFERENCE: 108074-00023

CURRENT APPLICATION NUMBER: US/10/084,507B

CURRENT FILING DATE: 1998-12-30

PRIOR PILING DATE: 1998-12-30

PRIOR PILING DATE: 1998-12-30

PRIOR PILING DATE: 1998-12-30

PRIOR PILING DATE: 1998-12-30

PRIOR PLING DATE: 1998-12-30

PRIOR PLING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 60/070,185

PRIOR PLING DATE: 1998-11-25

PRIOR APPLICATION NUMBER: 60/070,185

PRIOR PLING DATE: 1998-11-23

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 17

LENGTH: 353
APPLICANT: Ping Tsui
TITLE OF INVENTION: EDG FAMILY GENE, HUMAN H218
FILE REFERENCE: GP-70431-C1
CURRENT APPLICATION NUMBER: US/09/771,063
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/150,650
PRIOR FILING DATE: 1998-09-03
PRIOR PILING DATE: 1998-04-23
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
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Pred. No. 9.7e-156;
1; Mismatches 1;
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; ORGANISM: HOMO SAPIENS
US-09-771-063-2
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APPLICANT: Masuda, Esteban
APPLICANT: Chu, Peter
APPLICANT: Pardo, Jorge
APPLICANT: Dardo, Jorge
APPLICANT: Li, Congfen
APPLICANT: Li, Congfen
APPLICANT: Ji and, Haoran
APPLICANT: Ji and, Yingpling
APPLICANT: Rigel Pharmaceuticals, Incorporated
TITLE OF INVENTION: EDG: Modulators of Lymphocyte Activation and Migration
TITLE REPRESENCE: 021044-000310US
CURRENT APPLICATION NUMBER: US/09/971,228
CURRENT FILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 201-04-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 3.4e-154;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09971228
Patent No. US20020155512A1
GENERAL INFORMATION:
APPLICANT: Liao, X. Charlene
APPLICANT: Masuda, Esteban
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APPLICANT: GASSENHUBER, Johann
APPLICANT: GASSENHUBER, Johann
TITLE OF INVENTION: EDGB RECEPTOR, ITS PREPARATION AND USE
TITLE TO INVENTION: EDGB RECEPTOR, ITS PREPARATION AND USE
FILE REPERSORE: 3005-147
CURRENT APPLICATION NUMBER: EP 116589.3
PRIOR FILING DATE: 2001-04-26
PRIOR FILING DATE: 2000-08-01
PRIOR PLILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN OF SEQ ID NOS: 9
SEQ ID NO 8
ILENGTH: 353
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Pred. No. 1.2e-155;
1; Mismatches 1;
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Pred. No. 3.4e-154;
1; Mismatches 3;
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Patent No. US20020099191A1
GENERAL INFORMATION:
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Best Local Similarity 99.4%;
Matches 351; Conservative
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ilarity 98.9%;
Conservative
                                  FEATURE:
NAME/KEY: MOD RES
LOCATION: (273)
OTHER INFORMATION: Leu or
                      ORGANISM: Homo sapiens
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Best Local Similarity
Matches 349; Conserv
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US-10-084-507B-17
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US-09-842-316-8
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Pred. No. 3.4e-154;
1; Mismatches 3;
  Score 1787; DB 4;
Pred. No. 3.4e-154;
1; Mismatches 3;
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APPLICANT: Bonini, James A.
APPLICANT: Bornesky, Beth E.
APPLICANT: Barowsky, Beth E.
APPLICANT: Salon, John A.
APPLICANT: Majorn, Ray
APPLICANT: Wilson, Amy
APPLICANT: Wagorny, Raisa
TITLE OF INVENTION: DNA Encoding Edg7 Receptor
FILE REFERENCE: 58230-a
CURRENT APPLICATION NUMBER: US/10/228,762
CURRENT PILING DATE: 2002-08-26
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: 09/253,998
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 20
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SEQ ID NO 19
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    98.8%;
98.9%;
Query Match
Best Local Similarity 98.9°
Matches 349; Conservative
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Best Local Similarity 98.9
Matches 349; Conservative
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US-10-228-762-19
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Publication No. US20030113798A1

GENERAL INFORMATION:

APPLICANT: LifeSpan Biosciences

APPLICANT: Burmer, Glenna C.

APPLICANT: Burmer, Glenna C.

APPLICANT: Burmer, Glenna C.

TILLE REFERENCE: 1920 4-4

FILLE REFERENCE: 1920 4-4

CURRENT APPLICATION NUMBER: US/10/225,567A

CURRENT PILING DATE: 2001-12-19

PRIOR PILIANG DATE: 2000-12-19

PRIOR FILING DATE: 2000-12-19

SOUTHARE: PATENTING DATE: 2000-12-19

SOUTHARE: PATENTING DATE: 3000-12-19

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                                                                                                          GENERAL INFORMATION:
APPLICANT: Shankar, Geetha
APPLICANT: Munning, Jason N
APPLICANT: Spencer, Juliet V
ITLE OF INVENTION: CHIMERIC G PROTEIN COUPLED RECEPTORS;
FILE REFERENCE: 10602-013-999
CURRENT APPLICANTION NUMBER: US/09/904,099
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
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Pred. No. 3.4e-154;
1; Mismatches 3;
                                                                        Sequence 33, Application US/09904099
Publication No. US20030119092A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.88;
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Best Local Similarity 98.9°
Matches 349; Conservative
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; ORGANISM: Homo sapiens
US-10-225-567A-508
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ORGANISM: Homo sapiens
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US-10-225-567A-508
                                                  -09-904-099-33
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HILLS OF INVENTION: EDG8 RECEPTOR, ITS PREPARATION AND USE TILLS OF INVENTION: EDG8 RECEPTOR, ITS PREPARATION AND USE FILES REPRENCE: 38005-147
CURRENT APPLICATION NUMBER: US/10/421,828
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: EP 116589.3
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 2000-04-26
NUMBER: OF SEQ ID NOS: 9
SOFTWARE: PLENCE PRIOR PRIOR PRIOR FILING DATE: 2000-04-26
NUMBER: PE PRIOR P
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; Sequence 7, Application US/10715117
; Publication No. US20040171037A1
; GENERAL IPPORMATION:
; APPLICANT: LI, JING
; APPLICANT: SIN, WUN CHEX
; APPLICANT: YANG, JIANXIN
; TITLE OF INVENTION: AMPLIFIED GENES INVOLVED IN CANG
; FILE REFERENCE: 38002-0062
; CURRENT FILING DATE: 2003-11-18
; PRIOR PELICATION NUMBER: 60/427,202
; PRIOR PILING DATE: 2002-11-19
; PRIOR FILING DATE: 2002-11-19
; PRIOR FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PATENTIN VET. 3.2
; SEQ ID NO 7.
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Pred. No. 3.4e-154;
1; Mismatches 3;
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Pred. No. 3.4e-154;
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98.9<del>8</del>;
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Best Local Similarity 98.9
Matches 349; Conservative
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US-10-715-117-7
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Best Local Similarity
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TYPE: PRT
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US-10-715-117-7
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Fublication No. US20030219808A1

GENERAL INFORMATION:

APPLICANT: KOSTENIS, Evi

APPLICANT: SIELGER, Karl-Ernst

APPLICANT: BIELGER, Martina

APPLICANT: DELENZE, Jean-Francois

APPLICANT: DELENZE, Jean-Francois

APPLICANT: DELENZE, Jean-Francois

APPLICANT: MACE, Sandrine

APPLICA
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Best Local Similarity 98.9%; Pred. No. 3.4e-154;
Matches 349; Conservative 1; Mismatches 3;
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Sequence 8, Application US/10421828

Publication No. US20030219874A1

GENERAL INFORMATION:

APPLICANT: KOSTENSIS, Eva
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Pred. No. 8e-154;
1; Mismatches 4; Indels
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APPLICANT: Derk J. Bergsma
APPLICANT: Nabil Elshourbagy
APPLICANT: Xiaotcong Li
APPLICANT: Xiaotcong Li
APPLICANT: Yiaotcong Li
APPLICANT: Jeffrey L. Mooney
APPLICANT: Jeffrey L. Mooney
APPLICANT: Ping Tsui
TITLE OF INVENTION: EGP-70431-C1
CURRENT APPLICATION NUMBER: US/09/771,063
CURRENT APPLICATION NUMBER: 09/150,650
PRIOR FILING DATE: 1998-09-03
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PSECSEQ for Windows Version 3.0
SEQ ID NO
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Publication No. US20030054452A1
APPLICANT: MUNROE, DONALD G.
APPLICANT: KAMBOJ. RAJENBER
APPLICANT: PETERS, DIANA
APPLICANT: ROSHESH, FATEMEH
                                                                                                                                                                                                                                  Sequence 4, Application US/09771063; Patent No. US20010034331A1; GENERAL INFORMATION:
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Best Local Similarity 98.6%;
Matches 348; Conservative
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US-10-084-507B-21
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| Publication No. US20050153289A1
| GENERAL INFORMATION:
| APPLICAINT: Takeda Chemical Industries, Ltd.
| TITLE OF INVENTION: Method of Analyzing Gene Expression
| FILE REFERENCE: P02-0155PC;
| CURRENT APPLICATION NUMBER: US/10/498,848
| CURRENT FILING DATE: 2004-06-14
| PRIOR PIPLICATION NUMBER: UP 2001-382053
| PRIOR FILING DATE: 2001-12-14
| PRIOR FILING DATE: 2002-06-15
| PRIOR FILING DATE: 2002-01-12
| PRIOR FILING DATE: 2002-01-15
| PRIOR FILING DATE: 2002-11-12
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Pred. No. 3.4e-154;
1; Mismatches 3;
1; Mismatches
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Best Local Similarity 98.9
Matches 349; Conservative
  349; Conservative
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US-10-498-848-46
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US-10-498-848-46
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89.9%; Score 1625.5; DB 4; Length 352;
Best Local Similarity 89.5%; Pred. No. 1.8e-139;
Matches 316; Conservative 14; Mismatches 22; Indels 1;
      VYAS, TEJAL B.
                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Rattus sp.
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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                                OM protein - protein search, using sw model
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                                                                                                                                                                                                                                        UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match
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| 326 2 Q9BF72 SORAR<br>326 2 Q99NQ9 HYDHY<br>326 2 Q9BF75 MYRTR<br>326 2 Q9BF76 TAMTE<br>326 2 Q9BF76 TAMTE<br>326 2 Q9BF79 CHOHO<br>326 2 Q9BF79 CHOHO<br>326 2 Q99F79 CHOHO<br>325 2 Q99NR9 TAMST<br>325 2 Q9NR9 TAMST<br>326 2 Q9BR66 ELERU<br>326 2 Q9BR66 ELERU<br>326 2 Q9BR66 ELERU<br>326 2 Q9BR65 MYAP<br>327 2 Q9BR66 MEGLY<br>328 2 Q9BR66 ELERU<br>328 2 Q9BR66 ELERU | Q9bf72 sorex arane | Qayndy nyarocnoeru | Q9D1/3 myrmecopnag<br>Q9Df76 tamandua te | •            | Q9bf74 erinaceus c |              | Q99nr5 mus musculu |              | _            | Q8mk86 megaderma l |              | Q9bf65 orycteropus | Q9bf41 panthera on |
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|  | Q9BF72_SORAR       | OSSNOS HYDHY       | U9BF/5 MIKIK<br>O9BF76 TAMTE             | Q99NR3 EREDO | Q9BF74 ERICO       | 09ВЕ79 СНОНО | Q99NR5 MOUSE       | Q91XR2_CAVPO | Q99NR9_TAMST | Q8MK86 MEGLY       | Q9BF66 ELERU | Q9BF65 ORYAF       | Q9BF41_PANON       |
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## ALIGNMENTS

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HEBOLT. 1

BEDGS HUMAN

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DT 29-MAR-2004 (Rel. 43) Created)

DT 29-MAR-2004 (Rel. 43) Created)

DT 29-MAR-2004 (Rel. 43) Last sequence update)

DT 29-MAR-2004 (Rel. 47) Last sequence update)

DT 29-MAR-2006 (Rel. 47) Last sequence update)

DT 29-MAR-2006 (Rel. 47) Last sequence update)

DT 29-MAR-2004 (Rel. 47) Last sequence update)

DT 29-MAR-2006 (Rel. 47) Last sequence update)

DT 29-MAR-2006 (Rel. 47) Last sequence update)

DG (Sphingosine 1-phosphate receptor Edg-5) (SIP Feceptor Edg-5)

DG (Sphingosine 1-phosphate receptor Edg-5) (SIP Feceptor Edg-5)

CRAPATION (Rel. 47) Last sequence and the sequence of the sequenc
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NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/63; TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                 QBC3Q7_MOUSE PRELIMINARY;
Q8C3Q7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001)
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                                                                                                                                                                                             s Swiss-Prot entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the BYML outstation -Buropean Bioinformatics Institute. There are no restrictions on its as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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FUNCTION: Receptor for the lysosphingolipid sphingosine 1-phosphate (SIP). SIP is a bloative lysophospholipid that elicits diverse physicalogical effect on most types of cells and tissues. When expressed in rat HTC4 hepatoma cells, is capable of mediating SIP-induced cell proliferation and suppression of apoptosis. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPROUGE:

( InterPro; IPROUGE: 5...

R InterPro; IPROUGE: 5...

DR PRINTS; PROUGE: 7tm 1.1

DR PRINTS; PROUGE: 5...

DR PRINTS; PROUGE: 5...

DR PROSTE: PSOUGE: 6...

PROSTE: PSOUGE: 6...

DR PROSTE: PSOUGE: 6...

DR PROSTE: PSOUGE: 6...

DR PROSTE: PSOUGE: 6...

Multigene family; Palmitate; Receptor; Transmembrane.

TOPO_DOM 1 34 Extracellular (Potential).

TOPO_DOM 35 59 1 (Potential).

TOPO_DOM 35 59 1 (Potential).

TOPO_DOM 35 59 1 (Potential).

TOPO_TOWN

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S-palmitoyl cysteine (By similarity).
N-linked (GlcNAc. . .) (Potential).
F -> S (in Ref. 1).
G -> V (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO:0004330; F:G-protein coupled receptor activity; TAS.
GO:00018289; F:lipid binding; TAS.
GO:0001817; P:activation of MAPR; TAS.
GO:000186; P:G-protein coupled receptor protein signalin.
GO:0009284; P:positive regulation of cell proliferation; TAS.
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Pred. No. 4.7e-114;
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Extracellular (Potential).
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                                                                                                                                                                                                                                                                                                                                     EMBL; AF034780; AAC98919.1; -; mRNA.
EMBL; AY52688; AAP20652.1; -; Genomic_IEMBL; BC069598; AAH69598.1; -; mRNA.
Ensembl; ENSG00000175898; Homo saplens.
HGNC; HGNC;3169; EDG5.
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318
353 AA;
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TOPO DOM
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C STRAIN=C57BL/61 TISSUE-Lung;

XA KARAI J., Shihadawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Xa Arakawa T., Shihadawa A., Shibata K., Xoshino M., Itoh M., Ishii Y.,

A Arawa T., Shihadawa A., Shibata K., Xonno H., Adachi J., Fukuda S.,

A Arawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kanukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburar M., Batalov S., Casavant T.,

Richmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Richmann W., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Ronstein M.J., Bult C., Fletcher C., Fujita M., Mariya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodfiguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                300
                                                                                   240
                                                                                                                                                                                                                                      Ol-MAR.2003 (TrEMBLrel. 23, Created)
01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
library, clone:0430039A03 product:endothelial differentiation,
sphingolipid G-protein-coupled receptor, 5, full insert sequence
(Endothelial differentiation, sphingolipid G-protein-coupled receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of
TVL.PL.YAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
                                                 TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
                                                                                                                                                                                241 VFIVCWLPAFSILLLIDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CS7BL/6J; TISSUE=Lung; MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninoi P., Hayashizaki Y.; Hayashizaki Y.; High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                           301 RPLQCWRPGVGVQGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353
                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection.";
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Madan A., Rodrigues S., Sanchez A.,

Bakesley R.W., Touchman M., Madan A., Rodrigues S., Sanchez A.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schent J.E., Jones S.J.M., Marra M.A.;

Rodriguez C.N., Grimwood J., Schmutz J., Myers R.M.,

Generation and initial analysis of more than 15,000 full-length human

R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUE=Lung;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Katoh H., Kawai J., Kojima Y., Miyazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsaco N., Oksaco N., 
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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-!- VBUSCELIDIAR LOCATION: Integral membrane protein (By similarity).
EMBL; AKOB5114; BAC39368.1; -; mRNA.
EMBL; BC096760; AAH96760.1; -; mRNA.
                                                                                                                                                                                                STRAIN=C57BL/G5; TISSUE=Lung;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawii J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
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GO;0007610; P:behavior; IMP.
InterPro; IPR004063; EDG5_receptor.
InterPro; IPR004061; SPCR_Rhodpsn.
InterPro; IPR004061; S1P_receptor.
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61 NSKFHSAMYLFLGNLAASDILAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
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Sphingosine 1-phosphate receptor Edg-5) (G-protein coupled receptor H218) (AGRIB) (Endochelial differentiation G-protein coupled receptor F18) (AGRIB) (Endochelial differentiation G-protein coupled receptor 5) (Sphingosine 1-phosphate receptor 2) (S1P2)
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MEDLINE=9437334; PubMed=8087418; DOI=10.1006/mcne.1994.1024;
Maclennan A.J., Browe C.S., Gaskin A.A., Lado D.C., Shaw G.;
"Cloning and characterization of a putative G-protein coupled receptor potentially involved in development.";
                                                                                                                                                                                                                                                                                                                                            1 MGGLYSEYLNPEKVLEHYNYTKETLDMQETTSRKVASARIIILCCAIVVENLLVLIAVAR
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
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MEDLINE=93176155; PubMed=8382486;
Okazaki H., Ishizaka N., Sakurai T., Kurokawa K., Goto K., Kumada M.,
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                                                                                                                                Transducer; Transmembrane
                                                                                                                                                                                                         DB 2; Length 352;
                   PRINTS; PRO1525; EDGSRECEPTOR.
PRINTS; PR0237; GPCRRMODOPSN.
PRINTS; PR01523; SIPRECEPTOR.
PROSITE; PS50062; GPROTEIN_RECEP_ FI_2; 1.
G-profein coupled receptor; Receptor; Trans G-profein S2 AA; 38829 MW; 6A3E426B0FE54406 CRC64;
                                                                                                                                                                                                                                  ; Pred. No. 2.1e-102; 13; Mismatches 21;
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                                                                                                                                                                                                         90.2%; Score 1631.5;
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PF00001: 7tm 1: 1
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TISSUE=Brain;
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240 240

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241 VPIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
                                                                                                                                                                                                                                   241 VFIICWLDAFSILLLDSTCPVRACPVLYKAHYFFAFATINSLLNPVIYTWRSRDLRREVL 300
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  61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGPVTLSLTPLQWFAREGSAFITLSASV 120
                                                                1 MGGLYSEYLNPEKVQEHYNYTKETLDMQETPSRKVASAFIIILCCAIVVENLLVLIAVAR
                                          FSLLAIAIBERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sclurognathi;
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Okazaki H., Ishizaka N., Sakurai T., Kurokawa K., Goto K., Kumada M.,
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Submitted (MGG-1998) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity)
EMBL; AB016931; BAA32454.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                    301 RPLQCWRPGVGVQGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353
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GO; GO: 0001619; F: lysosphingolipid and lysophosphatidic acid ...
GO; GO: 0001619; F: lysosphingolipid and lysophosphatidic acid ...
GO; GO: 000186; P: lysosphingolipid and lysophosphatidic acid ...
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000276; GPCR_Rhodpsn.
PRINTS; PR01525; EGGSRECEPTOR.
PRINTS; PR01525; EGGSRECEPTOR.
PRINTS; PR01525; GPCRRHODOPSN.
PRINTS; PR01525; GPCRRHODOPSN.
PRINTS; PR01525; GPCRRHODOPSN.
GPROSITE; PS50262; GPROTENN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane.
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89.5%; Pred. No. 5.5e-102;
ive 14; Mismatches 22; Indels
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Last annotation update)
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Matches 316; Conservative
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13-SEP-2005 (
13-SEP-2005 (
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                                                                                                                                         Pubmed=1038339; DOI=10.1074/jbc.274.27.18997;
Ancellin N., Hla T.;
Ancellin Darmacological properties and signal transduction of the sphingosine 1-phosphate receptors EDG-1, EDG-3, and EDG-5.";
J. Biol. Chem. 274:18997-19002(1999).
-! FUNCTION: Receptor for the lysosphingolipid sphingosine 1-phosphate (SIP). SIP is a bloactive lysophospholipid that elicits diverse physiological effect on most types of cells and tissues.
-! SUBCELLUIAR LOCATION: Integral membrane protein.
-! TISSUE SPECIFICITY: Expressed in all developing tissues with highest levels detected in primitive, transformed cells. Relative abundance: lung > kidney = skin = gut > spleen > brain > liver.
-! SIMILARITY: Belongs to the G-protein coupled receptor I family.
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MEDLINE=98072391; PubMed=9409733; DOI=10.1016/S0014-5793(97)01301-X; An S., Bleu T., Huang W., Hallmark O.G., Coughlin S.R., Goetzl E.J.; "Identification of cDNAs encoding two G protein-coupled receptors for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
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S-palmitoyl cysteine (By similarity).
N-linked (GlcNAc. . ) (Potential).
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PRINTS; PR01525; BDGSRECEPTOR.

PRINTS; PR01523; GPCRRHODOPRN.

PROSITTE; PS00237; GPROTEIN RECEP F1 1; FALSE_NEG.

PROSITE; PS00262; G_PROTEIN RECEP_F1 2; 1.

G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
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89.5%; Pred. No. 5.5e-102;
ive 14; Mismatches 22; Indels
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2 (Potential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
5 (Potential).
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7 (Potential).
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9C933A18E756CE1E CRC64;
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PIR; JC1465; JC1465.
Ensembl; ENSRNOG00000020653; Rattus norvegicus.
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GO; GO:0004930; F:G-protein coupled
InterPro; IPR004063; BDG5_receptor.
InterPro; IPR004063; GPCR_Rhodpsn.
InterPro; IPR004061; SIP_receptor.
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                                                                                                                            PHARMACOLOGICAL CHARACTERIZATION,
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                                                                                   'EBS Lett. 417:279-282(1997).
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Matches 316; Conservative
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NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGPVTLSLTPLOWFAREGSAFITLSASV 120
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01-0CT-1996 (Rel. 34, Created)
29-MAX-2004 (Rel. 43, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Sphingosine 1-phosphate receptor Edg-5 (SIP receptor Edg-5)
(Lysophospholipid receptor B2) (Endothelial differentiation G-protein
coupled receptor 5) (Sphingosine 1-phosphate receptor 2) (SIP2).
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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MEDLINE=99132310; PubMed=9931453; DOI=10.1016/S0378-1119(98)00589-7;
Zhang G., Contos J.J.A., Weiner J.A., Fukushima N., Chun J.;
"Comparative analysis of three murine G-protein coupled receptors activated by sphingosine-1-phosphate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 RPLLCWRQGKGATG-RRGGNPGHRLLPLRSSSSLERGLHMPTSPTFLEGNTVV 352
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Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L.,
Copeland N.G., Jenkins N.A.;
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Ensembl; ENSMUSG00000043895; Mus musculus

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GO; GO:0007610; P:behavior; IMP.
InterPro; IPR004063; BDG5 receptor.
InterPro; IPR004061; BDG5 receptor.
InterPro; IPR004061; BDG5 receptor.
InterPro; IPR004061; SIP_receptor.
InterPro; IPR004061; Ttm 1; 1.
PRINTS; PR01523; EDG5RECEPTOR.
PRINTS; PR01523; SIPRECEPTOR.
PROSITE; PS00237; G_PROTEIN RECEP_F1_1; PARTIAL.
PROSITE; PS002262; G_PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
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Cytoplasmic (Potential).

Extracellular (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

Extracellular (Potential).

Sytoplasmic (Potential).

Cytoplasmic (Potential).

Spalmitoyl cyteine (By similarity)

N-linked (GlCNAc. . .) (Potential).

P -> S (In Ref. 2).

H -> K (In Ref. 2).

H -> K (In Ref. 2).
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29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
29-MAR-2005 (Rel. 47, Last annotation update)
Sphingosine 1-phosphate receptor Edg-5 (SIP receptor Edg-5)
(Sphingosine 1-phosphate receptor 2) (SIP2).
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; Pred. No. 8.7e-102;
13; Mismatches 22;
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                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                      NUCLECTIDE SEQUENCE, AND VARIANTS MIL HIS-150 AND CYS-167.
MEDILINE-20365730; PubMed=10910360; DOI=10.1038/35018092;
Kupperman B., An S., Osborne N., Waldron S., Stainier D.Y.R.;
M. sphingosine-1-phosphate receptor regulates cell migration during vertebrate heart development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (Potential).
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 (Potential).
Extracellular (Potential)
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Cytoplasmic (Potential).
             rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF260256; AAF88001.1; -; mRNA.
Ensembl; ENSDARG0000009719; Danio rerio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZFIN, ZDB-GENE-020123-2; edg5.
InterPro; IPR000987; EDG1receptor.
InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR004061; SIP_receptor.
Pfam; PF000001; 7tm_1; 1.
                                                                                                                                                                                      Nature 406:192-195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
78
87
108
1128
1149
1167
1188
Name=edg5;
Brachydanio
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TRANSMEM
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234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 VIVLGVFIICWLPAFTILLLDTSCKWKQCPILNNAGIFFSFATLNSALNPLIYTLRSKD 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 TLSASVFSLLAIAIERHVAIAKVKLYGSDKSCRMLLLLIGASWLISLVLGGLPILGWNCLG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
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EMBL; AF289992; AAR83087.1; -; mRNN.

GO; GO:0016621; C:integral to membrane; IEA.

GO; GO:0001619; F:lyesephingolipid and lysophosphatidic acid . . .; IEA.

GO; GO:0001819; P:ryeseptor acitivity; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

GO; GO:0007186; P:signal transduction; IEA.

InterPro; IPR004063; EDG5_receptor.

InterPro; IPR004061; GPCR Rhodpsn.

InterPro; IPR004061; SIP_receptor.

FFA.

5 (Potential).
Cytoplasmic (Potential).
6 (Potential).
Extracellular (Potential).
7 (Potential).
Cytoplasmic (Potential).
S-palmitoyl cysteine (By similarity).
N-linked (GlcNAc. . .) (Potential).
R -> H (in mil; allele m93; lack of S1P-mediated signaling).
R -> C (in mil; allele te273; lack of S1P-mediated signaling).
R > C (in mil; allele te273; lack of S1P-mediated signaling).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 HLEACSTVLPLYAKHYVLCVVTIPSIILLAVVALYVRIYCVVRSSHADMAAPQTLALLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SLYSEYLNPNKVQEHYNYTKE-----TLETQETTSRQVASAFIVILCCAIVVENLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 LIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Endothelial differentiation sphingolipid G-protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cavia porcellus (Guinea pig).
Bukaryota, Metazooa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=hartley; TISSUE-Myenteric plexus;
Segura B.J., Xiao L., Cowles R.A., Turner D.J., Logsdon C.D.,
Mulholland M.W.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.2%; Score 998; DB 1; Length 370; 58.2%; Pred. No. 1.5e-59; ive 52; Mismatches 73; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 MRKEFLRVLCCW-----GLLNCGRPPHRCMVPLKSSSSME 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 LRREVLRPLQCWRPGVGVGQRRRGGTPGHH-LLPLRSSSSLE 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 AA; 41777 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 58.2%
Matches 199; Conservative
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Q91XRO;
           235
275
275
275
289
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           215
236
255
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CARBOHYD
VARIANT
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TOPO DOM
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TRANSMEM
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       TRANSMEM
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62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVF 121
GSVTLRLTPVQWFAREGSAFITLSASVFSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIG 153
                                                  ASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSIILLAVVALYVRIY 213
                                                                214 CVVRSSHADMAAPQTLALLKTVTIVLGVFIVCWLPAFSILLLDYACPVHSCPILYKAHYL 273
                                                                                                                    Pongo pygnaeus (Orangutan).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GPVTLSLTPLQWFAREGSAFITLSASVFSLLAIAIERQVAIAKVKLYGSDKSCRMLMLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 SLYSEYLNPNKVQEHYNYT-KETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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PRINTS; PRO1148; EDGIRECEPTOR.
PRINTS; PRO1523; SIPRECEPTOR.
PRINTS; PRO1523; SIPRECEPTOR.
PROSTITS; PSO1237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Hypothetical protein; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.3%; Score 856; DB 2; Length 382; 51.1%; Pred. No. 5.9e-50;
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                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59; Mismatches
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PANTHER; PTHR19266:SF5; EDG1receptor; 1.
                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                          Hypothetical protein DKFZp469M1119.
Name=DKFZp469M1119;
                                                                                                                                                                                                                                                                                 01-FEB-2005 (TrEMBLrel. 29, 01-FEB-2005 (TrEMBLrel. 29, 01-FEB-2005 (TrEMBLrel. 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The German cDNA Consortium;
                                                                                                                                                                                                                                                       QSR7A1 PONPY PRELIMINARY;
QSR7A1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ransmembrane
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                                                                                                                                                                               FAVSTLNSLL 283
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TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 161; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              Pongo.
NCBI_TaxID=9600;
                                                      154
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                                                                                                                                                                                                       .; IEA.
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                                                                                                                                                                                          20 YTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARNSKFHSAMYLFLGNLAASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTRAIN-Sprague-Dawley/Had;
A Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001619; F:lysosphingolipid and lysophosphatidic acid . . .;
GO; GO:0007186; F:receptor activity; IEA.
R GO; GO:0007165; P:receptor activity; RSA.
R GO; GO:0007165; P:signal transduction; IEA.
R InterPro; IPR0004063; EDGS_receptor.
R InterPro; IPR004061; SIP_receptor.
R InterPro; PR004061; SIP_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00001; 7tm 1; 1.—PRINTS; PR01525; EDGSRECRPTOR.
PRINTS; PR01523; GPCRRHODOPSN.
PRINTS; PR01523; SIPRECEPTOR.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 PRINTS; PR01525; EDGSRECEPTOR.
PRINTS; PR00237; GPCRRHODDPSN.
PRINTS; PR01523; SIPRECEPTOR.
PROSITE; PS00237; G PROTEIN RECEP F1 1; UNKNOWN 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
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                                                                                                                                      Length 202;
                                                                                                                                  Query Match 51.5%; Score 912; DB 2; Length 20 Best Local Similarity 91.1%; Pred. No. 2.4e-55; Matches 184; Conservative 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 AA; 20718 MW; 3CA0A5C188E168B1 CRC64;
                                                                                              202 202
202 AA; 21836 MW; D9814EC85B42320A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative G-protein coupled receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 AA
                                                                                                                                                                                                                                                                                                                                                                         200 IILLAVVALYVRIYCVVRSSHA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 88.49
Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9ESKO_RAT PRELIMINARY;
Q9ESKO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                 NON TER
NON TER
SEQUENCE
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Query Match
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Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
A plokins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B commercin M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Tocahiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                        231 LLKTVTIVLGVFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTW 290
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                            134 SLLAIAIERYVTMLKMKLHNGSNNFRLFLLISACWVISLIGGGEPIMGWNCIGALSSCST
                                                                                   SLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACST
                                                                    ----SHADMAAPQTLA
                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 13, Last sequence update)
G protein-coupled sphingolipid receptor (EDG1 protein) (Endothelial differentiation, sphingolipid G-protein-coupled receptor, Name-CHEDG1; Synonyme=EDG1; ORFNames=RP4-575N6.1-001; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S., Newbert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W., Korn B., Zuo D., Hu Y., LaBaer J.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tigyi G.J. Sr., Wang D. Sr.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                    VLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRS-----
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                                                                                                                                                                                                                                                                                      382 AA
                                                                                                                                                                                   291 RSRDLRREVLRPLQC 305
                                                                                                                                                                                                    314 TNKEMRRAFIRIMSC 328
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                                                                                                                                                                                                                                                                                   Q9NYN8 HUMAN PRELIMINARY;
Q9NYN8; Q9BYY4;
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                       EMBL; AF233365; AA418650.1; -; mENA.

EMBL; AF23365; AA418650.1; -; mENA.

EMBL; CR541765.1; -; mENA.

EMBL; CR541269; CAG46585.1; -; mENA.

EMBL; CR541269; CAG47065.1; -; mENA.

EMBL; AL109741; CAI21861.1; -; Genomic_DNA.

ENGO; GO:00016019; F:1yeosphingolipid and lysophosphatidic acid . . .; I

ENGO; GO:000186; F:1yeosphingolipid and lysophosphatidic acid . . .; I

ENGO; GO:0007186; P:Grecter activity; IEA.

ENGO; GO:0007186; P:Grecter activity; IEA.

ENGO; GO:0007186; P:Grecter activity; ENG.

ENGL: CAIR ANG.

ENGL: CAIR ANG
                                                           -! - SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
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10-MAY-2005 (Rel. 47, Last sequence update)
Sphingosine 1-phosphate receptor Edg-1 (Sphingosine 1-phosphate receptor 1) (S1P1).
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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60; Mismatches 84
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Matches 159; Conservative
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                                                            A Lado D.C., Browe C.S., Gaskin A.A., Borden J.M., Maclennan A.D.;

T. Lado D.C., Browe C.S., Gaskin A.A., Borden J.M., Maclennan A.D.;

T. Cloning of the rat edg-1 immediate-early gene: expression pattern suggests diverse functions.";

Gene 149:311-336(1994).

-I. FUNCTION: Receptor for the lysosphingolipid sphingosine 1-phosphate (SIP). SIP is a bioactive lysophospholipid that elicits diverse physiological effect on most types of cells and tissues.

This inducible epithelial cell G-protein-coupled receptor may be involved in the processes that regulate the differentiation of endothalial cells. Seems to be coupled to the G(i) subclass of heteromeric G proteins (By similarity).

-I. SUBCELLULAR LOCATION: Integral membrane protein.

-I. DEVELOPMENTAL STAGE: First detected at embryonic day 15. At postnatal day 14 detected in skin, spleen, liver, kidney, heart, testicle, lung and brain. At adulthood is most abundant in brain.

-I. SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                    MEDLINE=95047498; PubMed=7959012; DOI=10.1016/0378-1119(94)90171-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphoserine (Potential).
S-palmitoyl. cysteine (By similarity).
N-linked (GlcMc. . . ) (Potential).
090BA6AEE09DB4F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0642; EDGIRECEPTOR.
PRINTS; PRO1148; EDGARECEPTOR.
PRINTS; PRO1148; EDGARECEPTOR.
PRINTS; PRO1148; EDGARECEPTOR.
PROSITE; PRO123; SIPRECEPTOR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Tanaducer; Transmembrane.
TOPO_DOM
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6 (Potential).
Extracellular (Potential).
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Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
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PIR; 153870; 153870.
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354
329
                          NUCLEOTIDE SEQUENCE.
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4

Gaps

Mismatches 103; Indels 14;

46.8%; Score 847; DB 1; 48.4%; Pred. No. 2.4e-49;

61;

Conservative

Query Match Best Local Similarity Matches 167; Conserv

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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemfer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heishe F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakealey R.W., Touchman J.W., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                        LLKTVTIVLGVFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTW 290
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                    62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVF
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                                                                                                                                                    SLLAIAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACST
                                                                                                                                                                                                                                  VLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRS------SHADMAAPQTLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
--- SIMILARITY: BELONGS to the G-protein coupled receptor 1 family.
EMBL, BC097938; AAH97938.1; -; mRNA.
InterPro; IPR000987; EDG1receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 31, Created)
(TrEMBLrel. 31, Last sequence update)
(TrEMBLrel. 31, Last annotation update)
differentiation sphingolipid G-protein-coupled receptor
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                                                                                                                                                                                                                                                                                                                                                                                                            315 TUKEMRRAFIRIISCCKCPNGDSAGKFKRPIIPGMEFSRSKSDNS 359
                                                                                                                                                                                                                                                                                                                                                                                      291 RSRDLRREVLRPLQCWR-PGVGVQGR-RRGGTPGHHLLPLRSSSS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q4V7F6 RAT PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Placenta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endothelial
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13-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Edg1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200004B16 product:endothelial differentiation sphingolipid G-protein-coupled receptor 1, full insert sequence (Endothelial differentiation sphingolipid G-protein-coupled receptor 1).
Name=Edg1;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SLYSEYLNPNKVQEHYNYT-KETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQVSDYGNYDIIVRHYNYTGKLNIGVEKDHGIKLTSVVFILLICCLIILENIFVLLTIWKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVF
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                Interpro; IRR000276; GECR_Rhodpsn.
Interpro; IRR000276; GECR_Rhodpsn.
Pfam; PF000017 Thm 1: 12 Frceptor.
PRINTS; PR00142; EDG1RECEPTOR.
PRINTS; PR01148; EDG2RECEPTOR.
PRINTS; PR01523; GEPRECEPTOR.
PROSITE; PS01237; G PROTEIN RECEP_F1 1; 1.
PROSITE; PS02237; G PROTEIN RECEP_F1 2; 1.
G-PROSITE; AS01246; G-PROTEIN RECEP_F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::::| :| :| :| :| 315 TNKEMRRAFIRIISCCKCPNGDSAGKFKRPIIPGMEFSRSKSDNS 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     46.8%; Score 847; DB 2; 48.4%; Pred. No. 2.4e-49;
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Q9DC35 MOUSE PRELIMINARY;
Q9DC35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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Asido T., Okazadi Y., Goldoci T., Den H., Kashawa T., Salto R., Kadechaman W., Gaarerdand T., Giels G., King B., Kochiwa H., A. Kadel H., Ashburner M., Battor S., Casavant T., Maniel D., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Carling L., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriff J.W., Sababi F., Sababi T., Basancha T., Sababi T., Basancha T., Sababi T., Bashi G., Marzarelli R., Rambarer P., R. Mordone P., Marchiomi L., Mahima J., Wambarer P., Mordone J., Manie J., Wambarer P., Mordone J., Manie J., Wambarer P., Mordone J., Manie J., Wambarer P., Mordone J., Wambarer P., Mordone J., Manie J., Wambarer P., Mordone J., Manie J., Wambarer P., Wam

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RESULT 14
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
KETAINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
KITAUSHORE R.L., Feingold B.A., Grouse L.H., Derge J.G.,
KILAUSHORE R.D., Colling F.S., Wagner L., Shemen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malle J.A., Gunarathe P.H.,
Norley W., McLany D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Norley W., Helton B., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human
                                     Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayateu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai C.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Eye;
Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0642; EBGZRECEPTOR.
PRINTS; PRO1148; EDGZRECEPTOR.
PRINTS; PRO1148; EDGZRECEPTOR.
PRINTS; PRO1153; GPCRAHODOPSN.
PROSITE; PSO0237; GPROTEIN RECEP_F1_1; UNKNOWN_1.
PROSITE; PSO0262; GPROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 382 AA; 42639 MM; SFE4C9A2BD65CB2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6; TISSUE=Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences."
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                      NUCLEOTIDE SEQUENCE
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VLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRS------SHADMAAPQTLA 230
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                                                                                                                                                                                                                                                     SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVF 121
                                                                                                                                                                                                                                                                                       SLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACST 181
                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
EMBL; BT021184; AAX31366.1; -; mRNA.
EMBL; BT021184; AAX3136.1; -; mRNA.
EMBL; BT021184; AAX3136.1; -; mRNA.
EMBL; BT021184; P:lysosphingolipid and lysophosphatidic acid . . .; IEA.
GO; GO:0001619; F:receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
                                                                                                                                                                                      73
                                                                                                                                                               14 SSVSDYGNYDIIVRHYNYTGKLNIGABKDHGIKLTSVVFILICCFIILENIFVLLTIWKT
                                                                                                                       3 SLYSBYLNPNKVOEHYNYT-KETLETOETTSROVASAFIVILCCAIVVENLLVLIAVARN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-WAY-2005 (TrEMBLrel. 30, Created)
10-WAY-2005 (TrEMBLrel. 30, Last sequence update)
10-WAY-2005 (TrEMBLrel. 30, Last annotation update)
Endothelial differentiation, sphingolipid G-protein-coupled receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-POOLEd;
MEDLINE-POOLEd;
MEDLINE-POOLEd;
MEDLINE-POOLEd;
MEDLINE-POOLEd;
MEDLINE-POOLED;
MEDLINE-POOLED;
MID T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T.,
Gass E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,
Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
Keele J.W.;
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle.";
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T.P.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                               14;
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   Length 382;
46.7%; Score 845; DB 2; Length 382, 48.4%; Pred. No. 3.3e-49; ive 61; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 RSRDLRREVLRPLQCWR-PGVGVQGR-RRGGTPGHHLLPLRSSSS 333
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      Query Match
Best Local Similarity 48.4%
Matches 167; Conservative
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QSBIPO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLKTVTIVLGVFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTW 290
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
Chromosome undetermined SCAP-751, whole genome shotgun sequence.
ORNames=GSTENG00004/94001,
Tetraodon nigroviridis (Green puffer).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii, Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea, Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                         Transducer; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 382;
GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR000997; EDG1receptor.

InterPro; IPR000277; EDG2 receptor.

InterPro; IPR000276; GGCR Rhodpsn.

InterPro; IPR004061; SIP receptor.

InterPro; IPR004061; SIP receptor.

InterPro; IPR004061; TM 12 receptor.

PANTHER; PR000017 74m 12 receptor.

PRINTS; PR00144; EDG1RECEPTOR.

RENINTS; PR01247; GPCRRHODOPSN.

RENINTS; PR012237; GPCRHODOPSN.

RENINTS; PR012237; GPROTEIN RECEP F1 1; 1.

RENINTS; PS02237; GPROTEIN RECEP F1 1; 1.

RENINTS; PS02625; GPROTEIN RECEP F1 1; 1.

REQUENCE 382 AA, 42742 MW; 31FCB6164ABB12C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
46.7%; Score 844; DB 2;
Best Local Similarity 50.5%; Pred. No. 3.8e-49;
Matches 159; Conservative 58; Mismatches 86
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Q4T9E2_TETNG PRELIMINARY;
Q4T9E2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. 1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
C. 1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
C. 1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
C. 1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
C. 1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
C. 1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CAF904901; BEGINE CEPTOR.
CAFBORO 17 - 1 Genomic_DNA.
CAFBORO 17 - 1 GENERAL CEPTOR.
CAFBORO 17 - 1 CAFBORO 17 - 1 CAFBORO 17 - 1 CAFBORO 17 CAFBORO 18 CAFBO
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Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
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NUCLEOTIDE SEQUENCE,
NUCLEOTIDE SEQUENCE,
Senoscope, Whitehead Institute Centre for Genome Research,
Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
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                                                                                                    the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
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Matches 174; Conservative
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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 4, 2005, 06:38:17; Search time 24.5 Seconds (without alignments) 1386.307 Million cell updates/sec Run on:

US-10-084-507B-22 1809 1 MGSLYSEYLNPNKVQEHYNY......LERGMHMPTSPTFLEGNTVV 353 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Description         | probable G protein | Edg-1 orphan recep | G protein-coupled | sphingosine 1-phos | G protein-coupled | G protein-coupled | lysophosphatidic a | melanocortin 3 rec | melanocortin recep | G protein-coupled | G protein-coupled | probable G protein | melanocortin recep | G protein-coupled | melanocortin recep | melanocortin-5 rec | melanocortin 1 rec | cannabinoid recept |        | melanocortin 5 rec | melanocortin recep | cannabinoid recept | MSH receptor - bov | melanocortin 1 rec | cannabinoid recept | melanocyte-stimula | melanocyte stimula | O)     | cannabinoid recept |
|---------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|
| ΩI                  | JC1465             | 153870             | A35300            | JC7559             | E48909            | JC5245            | JC5293             | S43850             | B46647             | 165990            | A55689            | S48697             | 836636             | S40454            | JC2193             | 149008             | S71420             | A33117             | A57055 | JC5592             | JN0764             | S70364             | S45708             | S70005             | \$17595            | S25581             | T12055             | A48978 | 836750             |
| DB                  | 2                  | ~                  | ~                 | ~                  | ~                 | ~                 | ~                  | N                  | 7                  | 8                 | N                 | ~                  | N                  | (7)               | N                  | ~                  | N                  | N                  | N      | N                  | N                  | ~                  | ~                  | 7                  | ~                  | 0                  | ~                  | ~      | 0                  |
| Length              | 352                | 383                | 381               | 362                | 180               | 378               | 364                | 323                | 360                | 362               | 330               | 363                | 323                | 330               | 325                | 372                | 314                | 473                | 332    | 325                | 325                | 347                | 317                | 314                | 472                | 315                | 317                | 412    | 360                |
| %<br>Query<br>Match | 89.9               | 46.8               | 46.2              | 45.2               | 44.7              | 42.5              | 28.0               | 19.5               | 19.3               | 19.2              | 19.1              | 18.8               | 18.7               | 18.6              | 16.9               | 16.7               | 16.7               | 16.6               | 16.6   | 16.3               | 16.1               | 16.1               | 16.0               | 15.9               | 15.8               | 15.8               | 15.7               | 15.7   | 15.7               |
| Score               | 1625.5             | 847                | 836.5             | 817.5              | 808               | 769               | 206                | 352.5              | 4                  | 348               | 345               | 339.5              | 338.5              | 336               | 305                | 302                | 301.5              | 300                | 299.5  | 295.5              | 291.5              | 290.5              | 290                | 288.5              | 286                | 285                | 284.5              | 284.5  | 284                |
| Result<br>No.       |                    | 8                  | e                 | 4                  | 'n                | 9                 | 7                  | <b>c</b> o         | 6                  | 10                | 11                | 12                 | 13                 | 14                | 15                 | 16                 | 17                 | 18                 | 19     | 20                 | 21                 | 22                 | 23                 | 24                 | 25                 | 26                 | 27                 | 28     | 29                 |

| adenosine receptor | G protein-coupled | A2 adenosine recep | melanotropin recep | melanocyte-stimula | adrenocorticotropi | adrenocorticotropi | alpha-1A-adrenergi | alpha-1A-adrenergi | G protein-coupled | alpha-1-adrenergic | alpha-1A adrenergi | adrenocorticotropi | adenosine A2a rece | 5-HT4S receptor - | serotonin 4 recept |
|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|
| A48974             | S18444            | I48095             | S29204             | 146416             | 152326             | JC4046             | JH0447             | 139369             | D30341            | A40491             | A38731             | C43265             | S68247             | S55550            | S55549             |
|                    |                   | ~                  | N                  | ~                  | ~                  | ~                  | ~                  | ~                  |                   | ~                  | ~                  |                    |                    | O1                | a                  |
| CA                 | ~                 | • •                |                    |                    |                    |                    |                    | •••                | N                 | •••                | •••                | N                  |                    | •••               |                    |
| 410 2              | 320 2             | 409                | 317                | 325                | 296                | 296                | 501                | 572                | 412 2             | 515                | 560                | 297 2              | 409                | 387               | 406                |
|                    |                   |                    |                    | 15.2 325           |                    |                    |                    |                    |                   |                    |                    |                    |                    |                   |                    |
|                    | 15.5              | 15.5               | 15.3               |                    | 15.0               | 15.0               | 15.0               | 15.0               |                   | 14.8               | 14.5               |                    | 14.3               | 14.1              |                    |

### ALIGNMENTS

| <br>RESULT 1 JC1465 probable G protein-coupled receptor - rat C;Species: Rattus norvegicus (Norway rat) C;Species: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004 | -Jul-2004                    |
|--|------------------------------|
| <br>C;Accession: JC1465<br>R;Akazaki, H; Ishizaka, N.; Sakurai, T.; Kurokawa, K.; Goto, K.; Kumada, M.; Takuwa,<br>H;Orhem Rionhva, Res. Commun. 190. 1104-1109. 1993                  | Kumada, M.; Takuwa, Y        |
| <br>A; Title: Molecular cloning of a novel putative G protein-coupled re A; Reference number: JC1465; MUID:93176155; PMID:8382486  | receptor expressed in t      |
| A,Accession: JC1465 A,Accession: JC1465 A,Molecule type: mRNA A,Residues: 1-352 < OKA>   |                              |
| A.Cross-references: UNIPROT:P47752; UNIPARC:UPI00000001D; GB:AB016931; NID:g3445557; A.Experimental source: aortic smooth muscle   | 16931; NID:93445557; PI      |
| C.Superfamily: G protein-coupled receptor edg-1<br>C.Reywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot  | ein; transmembrane prot      |
| F;35-59/Domain: transmembrane #status predicted <tm1></tm1>  |                              |
| <br>F:110-128/Domain: transmembrane #status predicted <tm3></tm3>  |                              |
| F;148-173/Domain: transmembrane #status predicted <tm4> F;190-210/Domain: transmembrane #status predicted <tm5></tm5></tm4>  |                              |
| F;234-255/Domain: transmembrane #status predicted <tm6> F;272-293/Domain: transmembrane #status predicted <tm7></tm7></tm6>  |                              |
| F;19/Binding site: carbohydrate (ABn) (covalent) #status predicted F;142,145,18,219,329,330,331,33Biding site: phosphate (Ser) (covalent)  | l<br>covalent) #status predi |
| <br>Onerv Match 89.9%; Score 1625.5; DB 2; Length 352;   | 3;                           |
| <br>Similarity 89.5%; Pred. No. 6.3e-125;<br>6; Conservative 14; Mismatches 22; Indels   | 1; Gaps 1;                   |
| Qy 1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR  | LLVLIAVAR 60                 |
| QETPSRKVASAF)  | LVLIAVAR 60                  |
| <br>Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTFVQWFARBGSAFITLLSASV  | AFITLSASV 120                |
| Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGPVTLSLTPLQWFAREGSAFITLSASV   | AFITLSASV 120                |
| <br>Qy 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS  | CLGHLEACS 180                |
| <br>DD 121 FSLLAIAIERQVAIAKVKLYGSDKSCRMLMLIGASWLISLILGGLPILGWNCLDHLEACS  | CLDHLEACS 180                |
| Qy 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG  | LKTVTIVLG 240                |
| <br>LLAIVALYVRIYFVVRSSH  | LKTVTIVLG 240                |
| <br>Qy 241 VFIVCWLPAFSILLLDYACPURSCPILYKAHYLFAVSTLNSLLNBVIXTWRSRDLRREVL  | SRDLRREVL 300                |
| <br>Db 241 VFIICWLPAFSILLIDSTCPVRACPVLXKAHYFFAFATLNSLINFYTWRSRDLRREVL  | SRDLRREVL 300                |

7

Gaps

11;

----APQTLAL 231

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A; Residues: 1-362 <IMA>
A; Across-references: UNIPARC: UPI00001788F3; GB: AF321294
C; Comment: This receptor, a G protein-coupled receptor, mediates sphingosine 1-phosphate
or also functions in the developing central nervous system in cell proliferation, apopto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sphingosine 1-phosphate receptor - zebra fish
N;Alternate names: endothelial differentiation gene 1 receptor
C;Species Brachydanio rerio (zebra fish)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7559
R;Im, D.S.; Ungar, A.R.; Lynch, K.R.
Biochem. Biophys Res. Commun. 279, 139-143, 2000
A;Title: Characterization of a zebrafish (Danio rerio) sphingosine 1-phosphate receptor
A;Reference number: JC7559; MUID: 20563813; PMID:11112429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 CFIACWAPLFILLILIDVACQTLTCSILYKAEWFLALAVINSAMPLIYTLTSNEMRRAFI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 NLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVFSLLAIAIERHVA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 KKFHRPMYYFIGNLALSDLLAGVAYTANLLLSGATTYKLTPAQWFLREGSMFVALSASVF 133
                                                                                                                                                                                                                                                                                   134 IAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLC 193
                                                                                                                                                           SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVF 121
                                                                                                                                                                                                                                                        SLLAIAIAERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACST 181
                                                                                                                                                                                                                                                                                                                                                                                                                                              LKTVTIVLGVFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWR 291
                                                                                            14 SSVSDYVNYDIIVRHYNYTGKLNISADKENSIKLTSVVFILICCFIILENIFVLLTIWKT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -ADMAAPQTLALLKTVTIVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 VQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARNSKFHSAMYLFLG
                                                               SLYSEYLNPNKVQEHYNYT-KETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 362;
                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: edg1
C;Superfamily: G protein-coupled receptor edg-1
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                       VLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMA---
No. 1.2e-60;
smatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.2%; Score 817.5; DB 3 45.4%; Pred. No. 3.9e-59
                     60; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 VVTIFSIILLAVVALYVRIYCVVRSSH---
  Pred.
49.78;
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Best Local Similarity 45.2%;
Matches 161; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 SRDLRREVLRPLQC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 NKEMRRAFIRIMSC 327
                     Conservative
Local Similarity
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                     Matches
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G protein-coupled receptor edg-1 - human

C; Species Homo sapiens (man)

C; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004

C; Accession: A35300

R; Hla, T: Maclagy T.

J; Balol. Chem. 265, 9308-9313, 1990

A; Title: An abundant transcript induced in differentiating human endothelial cells encoc

A; Reference number: A35300; MUD:90264425; PMID:2160972

A; Accession: A35300

A; Molecule type: mRNA

A; Crose-references: UNIPROT:P21453; UNIPARC:UP10000037801; GB:M31210; NID:g181948; PIDN:

C; Genetics:

A; Crose-references: GDB:127754; OMIM:131222

A; Map position: 22q13-22q13

C; Superfamily: G protein-coupled receptor_edg-1
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                                                                                                                                                                                                                                                                                                        expression pattern suggests
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane
                                                                                                                              Accession: 123870
Edg-1 orphan receptor - rat
C;Specides: Rattus norvegicus (Norway rat)
C;Specides: Rattus norvegicus (Norway rat)
C;Specides: Rattus norvegicus
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 153870
R;Lado, D.C.; Browe, C.S.; Gaskin, A.A.; Borden, J.M.; MacLennan, A.J.
Gene 149, 311-336, 1994
A;Title: Cloning of the rat edg-1 immediate-early gene: expression pattern sugge
A;Reference number: 153870; MUID:95047498; PMID:7959012
A;Reference number: 153870
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residus: preliminary;
A;Molecule type: mRNA
A;Residus: 1-383 - RESA
A;Cross-references: UNIPROY:P48303; UNIPARC:UPI0000129BD0; EMBL:U10303; NID:9595
C;Superfamily: G protein-coupled receptor edg-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLLAIAIERYITMLKWKLHNGSNSSRSFLLISACWVISLILGGLPIMGWNCISSLSSCST 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRS-----SHADMAAPQTLA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIKTVTIVLGVFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTW 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVF 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                          RPLOCWRPGVGVQGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THEMREAFIRIISCCKCPNGDSAGKFKRPIIPGMEFSRSKSDNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 847; DB 2;
Pred. No. 1.6e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.8%; Score 847; 48.4%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Addition Matches 167; Conservative
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A;Cross-references: UNIPROT:Q92633; UNIPARC:UPI000050403; GB:U80811; NID:g1857424; PID?
C;Superfamily: G protein-coupled receptor edg-1
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                                                                                                                                                                                                                                                                     93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nysophosphatidic acid receptor - human
Nysophosphatidic acid receptor - human
Nylternate names: Edg2 protein
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accesion: JC5293
R;An, S.; Dickens, M.A.; Bleu, T.; Hallmark, O.G.; Goetzl, E.J.
Biochem. Biophys. Res. Commun. 231, 619-622, 1997
A;Title: Molecular cloning of the human Edg2 protein and its identification
A;Contents: lung
A;Contents: lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melanocortin 3 receptor - mouse
C;Species: Mus musculus (house mouse)
C;Dacies 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S43850; S37153
R;Desarnaud, F.; Labbe, O.; Eggerickx, D.; Vassart, G.; Parmentier, M.
                                                                                                                                                   SKKYIAFCISIFTAILVTIVILYARIYFLVKSSSRKVANHNNSERSMALLRTVVIVVSVF
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                                                                                                                 AKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMA----APQTLALLKTVTIVLGVF
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AIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLY
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                                                                                                                                                                                                                                                                                                                                                        LQCWRPGVGVQGRRRGGTPGHHLL-PLRS-SSSLERGMHMP 341
                                                                                                                                                                                                                                                                                                                                                                                                                LVC---NCLVRGRGARASPIOPALDPSRSKSSSNNSSHSP 349
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A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
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C;Species: Homo sapiens (man)
B;Species: Homo sapiens (man)
B;
                                                                                                                                                                                              G protein-coupled receptor Gpcr13 - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: On-Dec-1995 #sequence_revision O1-Dec-1995 #text_change O9-Ju1-2004
C; Accession: E48909
R; Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G
Genomics 18, 175-184, 1993
A; Fitle: Identification, chromosomal location, and genome organization of mammalian G-pz
A; Reference number: A48909
A; Retens: Perliminary; nucleic acid sequence not shown
A; Status: preliminary; nucleic acid sequence not shown
A; Residues: 1-180 < WIL>
A; Residues: 1-180 < WIL>
Cross=references: UNIPROT:P52592; UNIPARC:UP10000029470; GB:L20334; NID:g438786; PIDN:C; Superfamily: G protein-coupled receptor
C; Keywords: G protein-coupled receptor
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   353
                                    305 KMLNC---GVCVQPSGKPSRP---IMGAEFSTSKSDNSSHPNKDEPEYSPRETIV 353
   RPLQCWRPGVGVQGRRRGGTPGHHLLPLRSSSSLERGMHMPT--SPTFLEGNTVV
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Pred. No. 1.2e-58;
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Best Local Similarity 91.1%;
Matches 164; Conservative
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ASSESS Decrees receptor 3 - human Grothernate names: Grotein-coupled receptor AC Grotein-coupled receptor AC Grotein-coupled receptor GPR3; orphan G-protein-coupled receptor AC C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: O3-Mar-1995 #stext_change 09-Jul-2004 C;Accession: A55689; S58521; C55733 R;Iismaa, T.P.; Kiefer, J; Liu, M.L.; Baker, E.; Sutherland, G.R.; Shine, J. Genomics 24, 391-394, 1994 A;Tiles: Isolation and chromosomal localization of a novel human G-protein-coupled receptor A;Reference number: A55689; MUID:95213036; PMID:7698767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P46095; UNIPARC:UPI000000DA4A; GB:L36150; NID:g598156; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R.; Heng, H.H.Q.; Marchese,
                                                                                                                                                                                                                                                                                                                                                                 G procein-coupled receptor 6 - human C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C; Accession: 165990
R; Heiber, M.; Docherty, J.M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng, H.H.Q.; Marche DNA, Cell Biol. 14, 25-35, 1995
A; Title: Isolation of three novel human genes encoding G protein-coupled receptors. A; Reference number: 153033; MUID:95134353; PMID:7832990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 CQVVWRHAHQIALQQHCLAPPHLAATRKGVGTLAVVLGTFGASWLP-FAIY-----CVVG 302
     240
                                                 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 SVTLRLTPVQWFAREGSAFITLSASVFSLLAIAIERHVAIAKVKLYGSDKS-CRMLLLIG 153
                              41 VILCCA---IVVENLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTL---LSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 ASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSIILLAVVALYVRIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 CVVRSSHAD------MAAPQTLALLK---TVTIVLGVFIVCWLPAFSILLLDYACPV-
     LCVVTIFSIILLAVVALYVRIYCVVR-----SSHADMAAPQTLALLK---TVTIVLG
                                                                                                    241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHY -- LFAVSTLNSLLNPVIYTWRSRDLR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -HSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV-LRPLQCWRPGVGVQGR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 SHEDPAVY-TYATLLPATYNSMINPIIYAFRNQEIQRALWLLLCGCFQSKVPFRSR 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
19.2%; Score 348; DB 2; Length 36
Best Local Similarity 34.1%; Pred. No. 6.6e-21;
Matches 101; Conservative 53; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-362 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: GDB:GPR6
A,Cross-references: GDB:371713; OMIM:600553
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A;Molecule type: DNA; mRNA
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                                                                                                                                                                                                      -REVL 300
                                                                                                                                                                                                                                                     347 FREIL 351
     192
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Biochem. J. 299, 367-373, 1994

A;Title: Molecular cloning, functional expression and pharmacological characterization A; Title: Molecular cloning, functional expression and pharmacological characterization A; Reference number: 843850; MUID:94226597; PMID:8172596
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-323 < ADES>
A; Cross-references: UNIPROT:P33033; UNIPARC:UPI0000004010; EMBL:X74983; NID:9400473; PIC; Superfamily: melanocortin receptor
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B46647
melanocortin receptor 3 - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 04-Sep-1998
C;Accession: 446647
R;Gantz, I.; Konda, Y.; Tashiro, T.; Shimoto, Y.; Miwa, H.; Munzert, G.; Watson, S.J.;
J. Biol. Chem. 268, 8246-8250, 1993
A;Title: Molecular cloning of a novel melanocortin receptor.
A;Reference number: A46647; MUID:93216807; PMID:8463333
A;Accession: B46647
A;Accession: B46647
A;Accession: compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-360 cGAN>
A;Cross-references: UniPARC:UPI00001789CB
A;Note: sequence extracted from NCBI backbone (NCBIP:129161)
C;Genetics:
A;Gene: GDB:MG3R
A;Cross-references: GDB:138780
A;Accession: 2043.2-2043.3
C;Superfamily: melanocortin receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VFLALGIVSLMENILVILAVVRNGNLHSPMYFFLCSLAAADMLVSLSNSLETIMIAVINS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSVTLRLTPVQWFAR--EGSAFITLSASVFSLLAIAIERHVAIAKVKLYGSDKSCR-MLL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YVRIYCVVR-----SSHADMAAPQTLALLK---TVTIVLGVFIVCWLPAFSILLLDY 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKVKLYGSDKSCR-MLLLIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLY--AKHYV 191
                                                                                                                                                                                                                                                                                                                                                         93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACPVHSCPILYKAHY -- LFAVSTLNSLLNPVIYTWRSRDLR---REVL 300
                                                                                                                                                                                                                                                       Length 323;
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                                                                                                                                                                                                                                                     19.5%; Score 352.5; DB 2; Length 34.0%; Pred. No. 2.5e-21; ive 52; Mismatches 93; Indels
                                                                                                                                                                                                                                                                            Best Local Similarity 34.0%
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32
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S40454
G protein-coupled receptor GPCR21 - m
C;Species: Mus musculus (house mouse)
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Matches 95; Conserv
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A; Residues: 1-330 <115>
A; Cross-references: UNIPROT: P46089; UNIPARC: UPI0000001624; GB: L32830; GB: L32831; NID: 960
R; Eggerickx, D: Denef, J: Labbe, O: Hayashi, Y: Refetoff, S:; Vassart, G: Parment
Biochem. J. 309, 837-843, 1995
A; Title: Molecular cloning of an orphan G-protein-coupled receptor that constitutively a
A; Reference number: S5821
A; Reference number: S58221
A; Reference number: S58221
A; Reference number: S58221
A; Reference number: S6821
A; Reference number: S6821
A; Residues: 1-330 < kgGo-
A; Cross-references: UNIPARC: UPI000001624; GB: K83956; NID: g1061125; PIDN: CAA58787.1; PID
R; Marchese, A: Docherty, J.M.; Nguyen, T:; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui, I
Genomics 23, 609-618, 1994
A; Residues: 1-292 cMAR>
A; Residues: A: Docherty, J.M.; MUID: 95154831; PMID: 7851889
A; Residues: 1-292 cMAR>
A; Cross-references: UNIPARC: UPI000016A113; GB: U13668; NID: g577416; PIDN: AAA64594.1; PID: C; Geneics:
A; Geneics: A; Gpscfamily: melanocortin receptor; transmembrane protein
C; Keywords: G protein-coupled receptor; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSI--ILLAVVAL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 AMDVVLCISGTLVSCENALVVAIIVGTPAFRAPMFLLVGSLAVADLLAGLGLVLHFAAVF 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSGSVTLRLTPVOWFAREGSAFITLSASVFSLLAIAIERHVAIAKVKLYGSDKS-CRMLL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YVRIYCVVRSSHADMAAPQTLAL------LKTVTIVLGVFIVCWLPAFSILLLDY 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
19.1%; Score 345; DB 2; Length 330;
Best Local Similarity 33.3%; Pred. No. 1.1e-20;
Matches 96; Conservative 49; Mismatches 107; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVLRPLQC 305
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18.8%; Score 339.5; DB 2;
Best Local Similarity 34.7%; Pred. No. 3.3e-20;
Matches 96; Conservative 51; Mismatches 95;
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12;

Gaps

35;

Indels

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C; Accession: A48254; S36636
R; Roselli-Rehfuss, L.; Mountjoy, K.G.; Robbins, L.S.; Mortrud, M.T.; Low, M.J.; Tatro, J. Proc. Natl. Acad. Sci. US.A. 90, 88856-8860, 1993
A; Title: Identification of a receptor for gamma melanotropin and other proopiomelanocort A; Reference number: A48254; MUID: 94022273; PMID: 8415620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-323 «ROS»
A; Cross-references: UNIPROT: P32244; UNIPARC: UPI000012ED4C; EMBL: X70667; NID: g396551; PID
A; Note: submitted to the EMBL Data Library, January 1993
A; Note: in Genbank entry RRMC3RA, release 113.0, the source is designated as Rattus ratt
C; Genetics:
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                                       213
                                                                                                                                                                                                                                                                   CVVRSSHAD------MAAPQTLALLK---TVTIVLGVFIVCWLPAFSILLLDYACPVH 262
                                                                                                                                                                                                                                                                                                                                                                                     250 CQVVWRHAHQIALQQHCLAPPHLAATRKGVGTLAVVLGTFGASWLP-FAIY-----CVVG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 VFLALGIVSLMENILVILAVVRNGNLHSPMYFFLLSLLQADMLVSLSNSLETIMIVVINS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 GSVTLRLTPVQWFAR--EGSAFITLSASVFSLLAIAIERHVAIAKVKLYGSDKSCRMLLL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209
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94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
                                                                                                               SVILRLIPVQWFAREGSAFITLSASVFSLLAIAIERHVAIAKVKLYGSDKS-CRMLLLIG
                                                                                                                                                                                                                              154 ASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSIILLAVVALYVRIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --SLIVAI------WVCCG---ICGVMFIVYSESKMVIVCLITMFFAMVLLMGTLY
VILCCA---IVVENLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLLLS---G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 VILCCAIV--VENLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLL----S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPTNPYCICYTAHFNTYLVLIMCNSVIDPLIYAFRSLEL-RNTFKEILCGCNGMNV 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: MG3-R
C;Superfamily: melanocottin receptor
C;Superfamily: melanocottin receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S--CPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRR 297
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llarity 32.1%; Pred. No. 3.5e-20;
Conservative 56; Mismatches 104;
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183
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C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Species: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004

C;Accession: Jo2193

R;Griffon, N.; Mignon, V.; Facchinetti, P.; Diaz, J.; Schwartz, J.C.; Sokoloff, P.

R;Griffon, N.; Mignon, V.; Facchinetti, P.; Diaz, J.; Schwartz, J.C.; Sokoloff, P.

A;Title: Molecular cloning and characteriation of the rat fifth melanocortin receptor.

A;Reference number: JC2193, MUID:94234987; PMID:8179577

A;Residues: 1-325 cRI>

A;Rolecule type: DNA

A;Residues: 1-325 cRI>

A;Roserences: UNIPROT:P35345; UNIPARC:UPI000012ED53; GB:L27081; NID:9435606; PIDN:
C;Keywords: G protein-coupled receptor; receptor; transmembrane protein
C;Keywords: G protein-coupled receptor; receptor; transmembrane #status predicted <TM1>
F;37-63/Domain: transmembrane #status predicted <TM2>
F;117-138/Domain: transmembrane #status predicted <TM3>
F;193-211/Domain: transmembrane #status predicted <TM5>
F;193-211/Domain: transmembrane #status predicted <TM5>
F;240-263/Domain: transmembrane #status predicted <TM5>
F;276-297/Domain: transme
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: $40454
R;Aseki, Uso, S.; Mizuno, R.; Nishimura, T.; Fujimura, H.; Nagai, Y.; Yanagihara, T
FEBS Lett. 336, 317-322, 1993
A;Title: Molecular cloning of a novel putative G protein-coupled receptor (GPCR21) which
A;Reference number: $40454
A;Refacence number: $40454
A;Nolecular preliminary
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Residues: 1-330 < SAE>
A;Cross-references: UNIPROT:P35413; UNIPARC:UPI0000025C17; GB:D21062; NID:9455487; PIDN:
C;Superfamily: melanocortin receptor
C;Keywords: G protein-coupled receptor; phosphoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 AMDVVLCISGTLVSCENALVVAIIVGTPAFRAPMFLLVGSLAVADLLAGLGLVLHFAADF 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 LSGSVTLRLTPVQWFAREGSAFITLSASVFSLLAIAIARHVAIAKVKLYGSDKS-CRMLL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 LIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSI--ILLAVVAL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 YVRIYCVVRSSHADMAAPQTLAL-----LKTVTIVLGVFIVCWLPAFSILLLDY 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 ICRIVC----RHAQQIALQRHLLPASHYVATRKGIATLAVVLGAFAACWLPFTVYCLLGD 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 AFIVILCCA---IVVENLIVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFV---ANTL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NYTKETLETQETTSRQVASAFIVILCCAIV--VENLLVLIAVARNSKFHSAMYLFLGNLA 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 18.6%; Score 336; DB 2; Length 330;
1 Similarity 32.3%; Pred. No. 5.7e-20;
93; Conservative 50; Mismatches 109; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258 ACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVLRPLQC 305
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Search completed: December 4, 2005, 06:52:58 Job time : 25.5 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description         | Aav28289 EDG-4 ami | Aay49904 Human EDG |          | Aab18889 Amino aci | Abp59285 Human Edg | 4        | Abu08813 Human EDG | Abp82010 Human sph | Adc40485 Protein o | 7 Human  | Add90760 Human Edg | Adh57161 Human end | 2 Human  | Ado29293 Human GPC | Ado57997 Human EDG | 2 Human  | Adp88359 Human EDG | Aay49905 Human EDG | Add11249 Human EDG | Adu92079 Human end | Aab03966 Murine ED | Aar58712 Fragment |          | Aay05492 Human EDG |
|-----------|---------------------|--------------------|--------------------|----------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|----------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|----------|--------------------|
| SUMMARIES | ID                  | AAY28289           | AAY49904           | AAY28288 | AAB18889           | ABP59285           | ABB98694 | ABU08813           | ABP82010           | ADC40485           | ADD11247 | ADD90760           | ADH57161           | ADJ62652 | AD029293           | AD057997           | AD022422 | ADP88359           | AAY49905           | ADD11249           | ADU92079           | AAB03966           | AAR58712          | AAW01663 | AAY05492           |
|           | DB                  | 18                 | 8                  | ~        | m                  | 9                  | 9        | 9                  | 9                  | 7                  | 7        | 7                  | œ                  | œ        | œ                  | æ                  | œ        | ω                  | N                  | 7                  | σ                  | m                  | ~                 | ~        | 7                  |
|           | Length              | 353                | 353                | 353      | 353                | 353                | 353      | 353                | 353                | 353                | 353      | 353                | 353                | 353      | 353                | 353                | 353      | 353                | 353                | 353                | m                  | m                  | 352               | 352      | 352                |
|           | &<br>Query<br>Match | 100.0              | 99.7               | 99.7     | 98.8               | 98.8               | 98.8     | 98.8               | 98.8               | 98.8               | 98.8     | 98.8               | 98.8               | 98.8     | 98.8               | 98.8               | 98.8     | 98.8               | 98.6               | 98.6               | 97.0               | 90.5               | 89.9              | 89.9     | 89.9               |
|           | Score               | 1809               | 1804               | 1803     | 1787               | 1787               | 1787     | 1787               | 1787               | 1787               | 1787     | 1787               | 1787               | 1787     | 1787               | 1787               | 1787     | 1787               | 1783               | 1783               | 1755               | 1631.5             | 1625.5            | 1625.5   | 1625.5             |
|           | Result<br>No.       |                    | 7                  | e        | 4                  | S                  | 9        | 7                  | 8                  | 6                  | 10       | 11                 | 12                 | 13       | 14                 | 15                 | 16       | 17                 | 18                 | 19                 | 20                 | 21                 |                   | 23       | 24                 |

| Rat      |          | Abu07712 Rat lysop | Abb98696 Rat Endot |          | Adp88361 Rat endot | Add48927 Rat Prote | Abb98695 Murine En | Ado29294 Mouse GPC | Adp29509 Human sec | Abp59289 Chimeric | Adg15135 Human 7 t | Aam96680 Human rep | Abb96585 Human tes | Adg15162 Human 7 t | Abp59281 Chimeric | Abp59280 Chimeric | Abp59279 Chimeric | Abg75679 Human Edg |          | Adx44606 Chimeric |
|----------|----------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|--------------------|----------|-------------------|
| AAW87790 | AAUU0305 | ABU07712           | ABB98696           | ABU61816 | ADP88361           | ADD48927           | ABB98695           | AD029294           | ADP29509           | ABP59289          | ADG15135           | AAM96680           | ABB96585           | ADG15162           | ABP59281          | ABP59280          | ABP59279          | ABG75679           | AD028787 | ADX44606          |
| 2.2      | 7        | _                  | 2                  | •        | 8 8                | •                  | 9 2                | 2 8                | 7 8                | 2 6               | 9                  | 4                  | 4                  | 4                  | 4 6               | 4 6               | 1 6               | 2 5                | 2 8      | 2                 |
| 35       | 352      | 35                 | 35                 | 35       | 35                 | 35                 | 352                | 35                 | 37                 | 372               | 26                 | 27                 | 27                 | 27                 | 38                | 384               | 39                | 36                 | 362      | 36                |
| 89.9     | 89.7     | 89.9               | 89.9               | 89.9     | 89.9               | 89.9               | 89.7               | 89.7               | 83.4               | 79.2              | 52.3               | 52.3               | 52.3               | 52.3               | 47.6              | 47.5              | 47.4              | 47.2               | 47.2     | 47.2              |
| 1625.5   | 1625.5   | 1625.5             | 1625.5             | 1625.5   | 1625.5             | 1625.5             | 1622.5             | 1622.5             | 1509.5             | 1432              | 946                | 946                | 946                | 946                | 860.5             | 858.5             | 858               | 854.5              | 854.5    | 854.5             |
| 25       | 56       | 27                 | 28                 | 59       | 30                 | 31                 | 32                 | 33                 | 34                 | 35                | 36                 | 37                 | 38                 | 39                 | 40                | 41                | 42                | 43                 | 44       | 45                |

#### ALIGNMENTS

EDG-4; polypeptide; receptor; inflammation; amino acid; G protein; lysolipid; immune response. Gupta AK; EDG-4 amino acid sequence encoded by clone pC3-hEDG4#36. Vyas TB, Kooshesh F, (ALLX ) ALLELIX BIOPHARMACEUTICALS INC. AAY28289 standard; protein; 353 AA Peters D, 97US-0070185P. 98US-0080610P. 98US-0109885P. 98WO-CA001195. 12-OCT-1999 (first entry) Kamboj R, WPI; 1999-430392/36. Homo sapiens W09935259-A1 30-DEC-1998; 30-DEC-1997; 03-APR-1998; 25-NOV-1998; 15-JUL-1999 g AAY28289; Munroe AAY28289 

New isolated lysolipid/EDG receptor useful in the treatment of asthma and rheumatoid arthritis.

Claim 7; Fig 16B; 120pp; English.

A novel isolated lysolipid (LL) receptor/EDG receptor (EDG-4). The LL/EDG receptors are involved in an inflammatory response signaling pathway and an apoptetic signaling pathway. They can be used for identifying sgonists or antagonists of NF-kB or IL-8 modulated EDG or LL receptors. Agonists can be used for upregulation of an inflammatory process condition or immune response. Antagonists can be used for the downregulation of an inflammatory process condition or immune response. The agonists and antagonists can also be used for controlling apoptosis in a cell comprising the LL/EDG receptor. A diagnostic test for aberrant expression of HEDG-4 can accelerate diagnosis and proper treatment of abnormal conditions of e.g. the heart, kidney, lung and testis. Specific examples

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                       include adult respiratory distress, asthma, rheumatoid arthritis, stroke, neurocrauma, Alzheimer's disease, endotozic shock, atheroselerosis, cardiac ischemia, acute pancreatitis, septic shock, psoriasis, acute cyclosporine nephrotoxicity, HIV/AIDS, myelodysplasia, cirrhosis of the liver, and early diabetic glomerulopathy, as well as lung damage following exposure to cigarette smoke, asbestos or silica. HEDG-4 specific antibodies, inhibitors, ligands or their analogs can be used as bioactive agents to treat inflammation or disease including viral, bacterial or fungal inflations, allergic responses, mechanical injury associated with trauma, hereditary diseases, lumphoma or carcinoma, or other conditions which activate the genes of kidney, lung, heart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
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conditions in which aberrant expression of HEDG-4 may play a role
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0;
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100.0%; Pred. No. 5.1e-177;
ive 0; Mismatches 0;
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98US-00150650.
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Best Local Similarity 100.
Matches 353; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 353 AA;
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03-SEP-1998;
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The present sequence is a human EDG family protein designated H218. H218 is used for diagnosing disease or its susceptibility in a subject related vis used for diagnosing disease or its susceptibility in a subject related with expression or activity of H218 by determining the presence or absence of mutation in the polymucleotide encoding H218 in the genome of the subject and/or analysing for the presence of H218 expression in carrier and derived from the subject. It is also used for treating subjects in need of enhanced activity or inhibition of H218 by administering an agonist or antagonist respectively. H218 can be used to treat abnormal conditions such as bacterial, fungal and viral infecting, particularly H1V-1 or 2, cancers, diabetes, obesity, anorexia, bulimia, asthma, conditions active have teather and absence acute heart failure, hypotension, hypertension, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, atroach, ulcers, asthma, allergies, benign prostatic hypertrophy, angraine, vomiting, psychotic, neurological disorders and dyskinesias can be treated. The H218 polynucleotide can also used for obtaining concluing H218. The difference in collating full-length clones encoding H218. The difference in collating full-length clones consuming the disease. It is also valuable for hormosome identification. The polypeptide is used for the identification of membrane bound or collars tructure based design of agonist, antagonist or inhibitor of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
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                                                                                                                                                          Novel human transmembrane receptor protein for use in treatment and
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Pred. No. 1.7e-176;
1; Mismatches 1; Indels (
                                                         Mooney JL,
                                                         Li X,
                                                         Lane P,
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                (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                 Claim 1; Page 29; 49pp; English.
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                                                         Bergsma DJ, Elshourbagy N,
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Matches 351; Conservative
                                                                                                                                                                              diagnosis of disease.
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                                                                                                                   N-PSDB; AAZ32488
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AC AAY2
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61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

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A apoptotic signaling pathway. They can be used for identifying pathway and an apoptotic signaling pathway. They can be used for identifying agonists or an apoptotic signaling pathway. They can be used for identifying agonists can be used for upregulation of an inflammatory process condition or immune response. The agonists and inflammatory process condition or immune response. The agonists and inflammatory process condition or immune response. The agonists and antagonists can also be used for controlling apoptosis in a cell comprising the LL/EDG receptor. A diagnostic test for aberrant expression of HEDG-4 can accelerate diagnosis and proper treatment of abnormal conditions of e.g. the heart, kidney, lung and testis. Specific examples of conditions in which aberrant expression of HEDG-4 may play a role include adult respiratory distress, asthma, rheumatorial arthritis, stroke, neurotrauma, Alzheimer's disease, asthma, rheumatorial arthritis, stroke, neurotrauma, Alzheimer's disease, asthma, rheumatorials, stroke, cardiac ischemia, acute pancreatitis, septic shock, psoriasis, stroke, liver, and early diabetic glomerulopathy, as well as lung damage to be used as the continuation of an indiplodies, inhibitors, ligands or their analogs can be used as the continuation of an indiplodies, inhibitors, ligands or their analogs can be used as the continuation of an indiplodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated lysolipid/EDG receptor useful in the treatment of asthma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A novel isolated lysolipid (LL) receptor/EDG receptor (EDG-4). The LL/EDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bloactive agents to treat inflammation or disease including viral, bacterial or fungal infections, allergic responses, mechanical injury associated with trauma, hereditary diseases, lymphoma or carcinoma, or other conditions which activate the genes of kidney, lung, heart, lymphoid or tissues of the nervous system
                                                                                                  EDG-4; polypeptide; receptor; inflammation; amino acid; G protein; lysolipid; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gupta AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vyas TB,
                                                            Predicted polypeptide product from human EDG-4 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peters D, Kooshesh F,
                                                                                                                                                                                                                                           /label= unknown
/note= "encoded by YTT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ALLX ) ALLELIX BIOPHARMACEUTICALS INC.
                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Fig 16A; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0070185P.
98US-0080610P.
98US-0109885P.
                                                                                                                                                                                                                                                                                                                                                                                           98WO-CA001195
                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rheumatoid arthritis
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                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                            WO9935259-A1
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25-NOV-1998;
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                     12-0CT-1999
                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Munroe DG,
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The present sequence represents an Edg polypeptide. The specification describes Edg4 and Edg5 polypeptides. The Edg4 gene is located on chromosome 19p12. The Edg polypeptides are receptors for 19p3 and sphingolipids, such as lysophosphatidic acid (LPA) and sphingosine 1-phosphate (S1P). The Edg receptor proteins are used for diagnosing an LPA or S1P mediator condition an individual. Edg4 and Edg5 polypeptides can be used in screening assays designed to determine the effects of a candidate bloactive agent on the expression and activity of Edg4 and Edg5 polypeptides, and the function of LPA and S1P. Nucleided sequences encoding Edg-4 and Edg-5 are useful as hybridisation probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. Nucleic acide which encode Edg4 or Edg5 or their medified forms can also be used to generate either transgenic animals or knock out animals. 240 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300 241 VFIVCWLPAFSILLLDYACPVHSCPLLYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300 Novel human polypeptide receptors for lysophospholipids and sphingolipids, native human Edg4, Edg5, mutant of Edg4 comprising extended polypeptide tail, used to screen agents that affect LPA and S1P 181 TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADWAAPQTLALLKTVTIVLG FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG RPLQCWRPGVGVGVGRRRGGTPGHHLLPLRSSSSLERGWHMPTSPTFLEGNTVV 353 Edg4, Edg5, lysophospholipid receptor, sphingolipid receptor, S1P, lysophosphatidic acid, LPA: sphingosine 1-phosphate, gene therapy. Amino acid sequence of the human Edg5 polypeptide. AAB18889 standard; protein; 353 AA. Claim 13; Fig 3; 67pp; English. 99US-00274752. 23-MAR-2000; 2000WO-US007649. (first entry) (REGC ) UNIV CALIFORNIA. WPI; 2000-638230/61. An S; N-PSDB; AAA96163. in gene therapy WO200056135-A2. 08-FEB-2001 Homo sapiens. 23-MAR-1999; 28-SEP-2000. activities. Goetzl EI, 301 AAB18889; 241 121 181 RESULT 4 8 셤 à 셤 Š 셤 ð g

Sequence 353 AA;

NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR 60

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1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR

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Gaps

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Score 1803; DB 2; Length 353; Pred. No. 2.1e-176; 1; Mismatches 1; Indels

99.7%;

Query Match Best Local Similarity 99.44 Matches 351; Conservative

9

9.3e-175;

Pred. No.

98.98;

Similarity

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                                                                                                                     NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
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                                                                                                                                                                                                                                                                                             VFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
                                                                                                                                                                                                                                                                                                                VFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVL 300
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                                                                                                                                     NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV
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                                                                                       1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
                                                                                                                                                                            FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
                                                                                                                                                                                                                                     TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
                                                             MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
                                  Gaps
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    Length 353;
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                                  3,
   Score 1787; DB 3;
Pred. No. 9.3e-175;
1; Mismatches 3;
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      98.8%;
98.9%;
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Query Match
Best Local Similarity 98.9
Matches 349; Conservative
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6; Length 353;

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                                                                                                                    NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
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                                        1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
              Gaps
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Endothelial Differentiation Gene; Edg-5; IgA nephritis.
             Indels
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              Mismatches
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06-SEP-2001; 2001JP-00270551.
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              Conservative
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Best Local Sim
Matches 349;
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Score 1787; DB 6;
Pred. No. 9.3e-175;
1; Mismatches 3;
    98.88;
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ABU08813 standard; protein; 353
          11-AUG-2003 (first entry)
              Human EDG-5 protein.
     ABU08813;
ABU08813
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Human; lymphocyte activation; lymphocyte migration; EDG-5; G-protein coupled receptor; GPCR; lymphocyte; T cell receptor; E cell receptor; E cell receptor; CD69; gene therapy; asthma; allergy; autoimmune disease; multiple sclerosis; scleroderma; pernicious anaemia; IDDM; insulin-dependent diabetes mellitus; tissue transplant; graft-versus-host disease; inflammation; infection. Ношо

US2002155512-A1. 24-OCT-2002

03-OCT-2001; 2001US-00971228. 18-APR-2001; 2001US-0284763P.

(RIGE-) RIGEL PHARM INC.

Identifying lymphocyte modulator activation/migration, by contacting an BDG G-protein coupled receptor polypeptide or cell having the polypeptide with compound and determining chemical/phenotypic effect of compound on cell. Jiang Zhao H, ບໍ ij Pardo J, Chu P, Masuda E, WPI; 2003-340852/32 Liao XC,

Disclosure; Fig 2; 70pp; English.

The invention discloses method for identifying a compound that modulates lymphocyte activation/migration. The method comprises contacting an EDG G-protein coupled receptor (GPCR) family polypeptide, or its fragment or a

determining the chemical/phenotypic effect of the compound upon the call algorithms are subject, by administering to the subject a therapeutically effective anount of an identified compound, an EDG polypeptide or a methods for modulating to the subject a therapeutically effective amount of an identified compound, an EDG polypeptide or a nucleic acid encoding an EDG, or its fragment, and for screening for mucleic acid encoding an EDG, or its fragment, and for screening for modulating T or B cell receptors of the lymphocytes a CDMA library, stimulating T or B cell receptors of the lymphocytes of CDG ocls surface expression and rescuing CDMAs that modulate (I ymphocyte activation. The method is useful for identifying a compound such as an antibody, antisense molecule, small organic molecule, cartivation or a sphingolipid analogue) that modulates lymphocyte activation or migration. The compounds identified are useful for the transment (e.g. gene therapy) of diseases such as such as such as a structum diseases such as multiple sclerosis, scleroderma, pernicious and tissue transplant such as graft-versus-host disease, acute and chronic inflammation, an infection such as viral, fungal, protozoal or bacterial infections and diseases in which activation of immune response and stimulation of lymphocyte migration is desired. The sequence and stimulation of lymphocyte migration is desired. The sequence G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regencation-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; 120 120 180 180 240 300 241 VFIVCWLPAFSILLIDYACPVHSCPILYKAHYFFAVSTLNSLINPVIYTWRSRDLRREVL 300 9 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS 1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVOWFAREGSAFITLSASV TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG VFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR Gaps comprising the polypeptide or its fragment with the compound, RPLOCWRPGVGGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353 ö Length 353; Indels Human sphingolipid receptor Edg5 protein SEQ ID NO:508. Score 1787; DB 6; Pred. No. 9.3e-175; 1; Mismatches 3; ż ABP82010 standard; protein; 353 98.8**%**; 98.9**%**; (first entry) Best Local Similarity 98.9 Matches 349; Conservative Sequence 353 AA; 04-MAR-2003 121 ABP82010; 61 61 121 181 181 241 301 Query Match RESULT 8 ABP82010 ठ 셤 Š 셤 δ a 8 셤 ò 셤 ઠે 엄

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181 TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG 240
                                                                                                                                                                                                               ADC40485 standard; protein; 353
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21-FEB-2002; 2002JP-00045104.
15-MAY-2002; 2002JP-00140111.
18-NOV-2002; 2002JP-00333769.
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Best Local Similarity 98.9
Matches 349; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino addids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR. and in the production of specific antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related disease, immunological-related clisease, coll respective diseases, or autoimmune diseases, growth-related disease, contextive disease, bacterial, fungal, protozoan or viral infections, atherosclerosis, bacterial, fungal, protozoan or viral infections, concertificities, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, pain, psoriasis, concertion and acute anxiety, depresention, achizohrenia, denetia, mental retardation, memory
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                                                                                                                                                                                                                                                                                                                            New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
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hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
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    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 523pp; English.
                                                                                                                                                                                                               (LIFE-) LIFESPAN BIOSCIENCES INC
                                                                                                                                                                                                                                               Brown JP;
                                                                                                                                               19-DEC-2001; 2001WO-US050107.
                                                                                                                                                                               19-DEC-2000; 2000US-0257144P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 349; Conservative
                                                                                                                                                                                                                                               Burmer GC, Roush CL,
                                                                                                                                                                                                                                                                               2003-046718/04.
                                                                                                                                                                                                                                                                                                                                                                               autoimmune diseases.
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                                                                                                                                                                                                                                                                                                N-PSDB; ABZ42860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 353 AA;
                                                                                WO200261087-A2
                                                Homo sapiens.
                                                                                                                08-AUG-2002
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collective quantitative analysis of the expression of a number of genes to identify those that are promoted or inhibited in a given cell or tissue. The genes are preferably gene families such as the G protein coupled receptor family, tyrosine oxidase receptor family, or ion channel gene family. The methods may be used in treatment of cancers, including prostate, ovarian, stomach, bladder, breast, and cancer of the intestines. EDG-1 and EDG-2 receptor agonists and antagonists may be used in the treatment and prevention of atherosclerosis, myocardial infarction, infarct or ischaemic disease of the brain. This sequence represents a protein of human EDG-5 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                       241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expression analysis; collective quantitative analysis; g protein coupled receptor; tyrosine oxidase receptor family; ion channel gene family; cancer; EDG-1; EDG-2 receptor; atherosclerosis; myocardial infarction; infarct; ischaemic disease; GPCR; human; EDG-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel method for gene expression analysis by
241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
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                                                                                                                                                 353
                                                                                                                                                                              ö
                                                                                                                                                 RPLOCWRPGVGVQGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for gene expression analysis for treatment of cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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', Ogi K;
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The present invention describes a method for identifying an increase in risk for Type II diabetes mellitus and/or venous thrombosis/pulmonary embolism, comprising determining the presence of amino acid exchange at postition 286 from Val to Ala in the EDGS protein. Also described: (1) a method for screening pharmaceuticals useful for treating and/or preventing type II diabetes and/or venous thrombosis/pulmonary embolism, where a call or call extract is used that contains EDGS with the amino acid exchange, or the Variation in the mucleotide sequence of EDGS corting the dosage of the pharmaceutical described above by testing the human cell for the presence of EDGS with the amino acid exchange, or the Variation in the nucleotide sequence of EDGS protein or the EDGS-286-AA, (3) a method of selecting patients who will respond type II diabetes and/or venous thrombosis/pulmonary embolism by testing the probe of the respective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying an increase in risk for Type II diabetes mellitus and/or venous thrombosis/pulmonary embolism comprises determining in a probe the presence of amino acid exchange at position 286 from Val to Ala in the
                                                                                                                                                          240
                                                                                                                                                                                             VFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Type II diabetes mellitus; venous thrombosis; pulmonary embolism; EDG5;
EDG5 V286A; antidiabetic; thrombolytic; gene therapy; human.
                                                                                                                                                                                                                  VFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVL
NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVOWFAREGSASITLSASV
                                                                    FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
                                                                                                                       TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
                                                                                                                                         PSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
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                                                                                                                                                                                                                                                                                      RPLQCWRPGVGGRRRVGTPGHHLLPLRSSSSLERGWHMPTSPTFLEGNTVV 353
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                                                                                                                                                                                                                                                                                                                                                                                         ADD11247 standard; protein; 353 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human EDG5 protein SEQ ID NO:3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Mace S;
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N-PSDB; ADD11248.
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          variation in the procession and the presence of EDGS protein or the EDGS-286-AA, and (4) a test kit for testing the presence of the amino acid exchange, or the variation in the nucleotide sequence of EDGS protein or the EDGS-286-AA. EDGS has antidiabetic and thrombolytic activities, and can be used in gene therapy. The methods are useful for identifying an increase in risk for type II diabetes mellitus and/or thrombosis/pulmonary embolism, and for screening pharmaceuticals useful for treating type II diabetes mellitus and/or venous thrombosis/pulmonary embolism. The methods are also useful for adapting the dosage of a pharmaceutical useful for treating the above diseases. The methods are useful for selecting patients who will respond to the pharmaceutical. The present sequence represents the human EDGS protein, which is used in an example
                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor; human; Edg5 receptor; gastrointestinal disorder; cardiovascular disorder; hypertension; diabetes; respiratory disorder; asthma; immunne disorder; cognitive disorder; memory disorder; obesity; pain; psychotic behaviour; affective disorder; migraine; cancer; AIDS; wound healing; ischaemia-reperfusion injury-related disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVL
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patient for the presence of EDG5 with the amino acid exchange, or the
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPLOCWRPGVGCRRRGGTPGHHLLPLRSSSSLERGWHMPTSPTFLEGNTVV 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                 Length 353;
                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                               Score 1787; DB 7;
Pred. No. 9.3e-175;
1; Mismatches 3;
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                                                                                                                                                                                                                                                                                  98.8%;
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                                                                                                                                                                                                                  from the present invention.
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                                                                                                                                                                                                                                                                                                                     Matches 349; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Edg5 receptor.
                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                     Sequence 353 AA;
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16-JUL-1999;
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                                                                                                                                                                                                                                                                                    Query Match
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(WILS/) (NAGO/)

HUAN/ BORO/) SALO/)

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This invention relates to a novel method for identifying an increase in risk for type II diabetes mellitus, venous thrombosis, pulmonary embolism of a combination thereof. Specifically, it refers to a the endothealal differentiation gene 5 (EDG5) located on chromosome 19p13.2, which encodes a G protein coupled receptor protein. The present invention describes an immunochemically reactive labelled antibody based kit that can be used to identify the Val286Au variation in the EDG5 protein encoded by a single nucleotide polymorphism. Furthermore, this allele for preventative treatments of the aforementioned diseases, as well as for adapting desage for patients, for drug screening purposes or for patient selection in phase or clinical studies. This polypeptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying an increase in risk for type II diabetes mellitus, venous thrombosis, pulmonary embolism or its combination in subject by determining whether amino acid residue at position 286 of EDG5 protein is
                                             3 protein coupled receptor; EDGS; type II diabetes mellitus;
venous thrombosis; pulmonary embolism; endothelial differentiation gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
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    Human endothelial differentiation factor 5 (EDG5) protein SegID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.8%; Score 1787; DB 8;
98.9%; Pred. No. 9.3e-175;
tive 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jacobs M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is the human EDG5 protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2.4; SEQ ID NO 3; 10pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Siegler K,
                                                                                                                                                                                                                                                                     21-MAR-2003; 2003US-00393870.
                                                                                                                                                                                                                                                                                                                09-AUG-2002; 2002US-0402305P.
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KOSTENIS E.
SIEGLER K.
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Matches 349; Conserv
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DELEUZE J.
RICARD S.
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                                                                                                                                   Homo sapiens
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(DELE/)
(RICA/)
(MACE/)
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                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid encoding a mammalian Edg7 receptor. The mammalian Edg7 receptor proteins and nucleic acid encoding the proteins are useful for diagnosing and treating an abnormality associated with the activity of the mammalian Edg7 receptors, ciaberes, respiratory disorder, asthma, immune disorder, hypertension, diaberes, respiratory disorder, asthma, immune disorder, hypertension, disorder, memory disorder, obseity, pain, psychotic behaviour, affective disorder, migraine, cancer, AIDS, wound healing, or ischaemia-reperfusion injury-related diseases. The nucleic acids and proteins are also useful cor developing and designing drugs with higher specificity and fewer side effects. The nucleic acid such encoding mammalian Edg7 receptors and antisense oligonucleotides complementary to the nucleic acid sequences. The methods are also useful for identifying agonists and antagonists of Edg7 receptors. The present sequence represents the amino acid sequence of the human Edg5 receptor.
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Edg7 receptors, useful for diagnosing and treating an abnormality
associated with the activity of the mammalian Edg7 receptor, e.g. asthma,
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Pred. No. 9.3e-175;
1; Mismatches 3;
                                                                                                                                                          Salon JA,
                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 19; 64pp; English
                                                                                                                                                          Borowsky BE,
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Best Local Similarity 98.9%;
Matches 349; Conservative
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                      HUANG L Y.
BOROWSKY B E.
SALON J A.
                                                                                                                                                                                                     WPI; 2003-829581/77
                                                                                                                                                                                                                                                                                                                   migraine or cancer.
BONINI J A.
                                                                                        WILSON A.
NAGORNY R.
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Ricard S;

Deleuze J,

240

TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG

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(first entry)

25-MAR-2004

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Indels

Length 353;

us-10-084-507b-22.rag

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Gaps

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3; Indels

Mismatches

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349; Conservative

Matches

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compound (by contacting a preferred target region of a nucleic acid molecule encoding EDGS with one or more candidate antisense compounds comprising at least an 8-nucleobase portion that is complementary to the preferred target region and selecting for one or more candidate antisense compounds that inhibit the expression of a nucleic acid encoding EDGS). The compound, composition and methods are useful for treating a disease or condition associated with EDGS, such as a hyperproliferative disorder, developmental disorder or a disease or condition arising from aberrant modulating the expression of EDGS. Experimental protocols are described but no results are given. The present sequence is the human EDGS protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a compound 8-80 nucleobases in length targeted to, and which specifically hybridises with a nucleic acid molecule encoding endothelial differentiation gene 5 (EDGS, a G protein coupled receptor, involved in development, wound healing, tissue regeneration, cellular proliferation, apoptosis, cancer, angiogenesis and inhibits the expression of EDGS, i.e. is an antisense (AS) oligonuclectide. Also included are a composition comprising the compound and a carrier or diluent and a method for screening an antisense
                       241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSKDLRREVL 300
VFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
                                                                                                                                                                                                                                                                                                                                                                                     Human; receptor; antisense gene therapy;
endothelial differentiation gene 5; EDG5; G protein-coupled receptor;
development; wound healing; tissue regeneration; cellular proliferation;
apoptosis; cancer; anglogenesis; inflammation;
hyperproliferative disorder; developmental disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense oligonucleotide targeted to nucleic acid encoding endothelial differentiation sphingolipid G-protein-coupled receptor 5, for treating cancer, developmental disorder or a condition arising from
                                                                              RPLOCWRPGVGVOGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353
                                                                                                     Human endothelial differentiation gene 5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 31-32; 50pp; English.
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Score 1787; DB 8; Length 353; Pred. No. 9.3e-175;

98.88;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                joint disorder; metabolic disorder; nutritive disorder; cancer; kidney disorder; netabolic disorder; lung disorder; breast disorder; overy disorder; uterus disorder; prostate disorder; breast disorder; stomach disorder; pancreas disorder; spleen disorder; thymus disorder; thyroid disorder; antiparkinsonian; antimanic; cytostatic; antiinflammatory; vasotropic; antianginal; antiarhythmic; follows, central nervous system; respiratory; antidarrhoeic; antidabetic; virucide; hepatotropic; antibacterial; antianaemic; antidabetic; dermacological; antiloer; antithyroid; antiallergic; anorectic; immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
                                                                                                                                                                                                                                                                     VFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSKDLRREVL
                                                                            61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV
                                                                                                                                         FSLLAIAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
                                                                                                                                                                                     TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
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                                                            NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse, neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; blood disorder; immune disorder; bone disorder;
                                                                                                                                                                                                                                                                                                                                  RPLOCWRPGVGVGVGRRRGGTPGHHLLPLRSSSSLERGWHMPTSPTFLEGNTVV 353
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Zeng H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J,
Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D,
                                                                                                                                                                                                                                                                                                                                                                                                                             AD029293 standard; protein; 353 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human GPCR EDG5, SEQ ID NO:394.
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compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.

Claim 151; SEQ ID NO 394; 542pp; English.

Human EDG5 receptor protein.

12-AUG-2004 (first entry)

ADO57997;

The invention relates to human and mouse G protein-coupled receptors (GPCRS) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids cof the invention; methods of screening for associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases, a transgenic compounds useful in the treatment of GPCR-related diseases, a transgenic compounds useful in the treatment of GPCR-related diseases, a transgenic computation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polynucleotides of the invention. The comprising a GPCR nucleic acids and proteins may comprising a GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, disrented and vectors of the adrenal gland; disorders of the colon or intestine (e.g., crohn's disease, diarrhoea, food poisoning or irritable bowel compression, disbetic neuropathy, Parkinson's disease or schizophrenia); macemia or leukaemia); muscular disorders (e.g., autoimmune disorders or myocardial infarction); muscular disorders (e.g., autoimmune disorders (e.g., atthirtie, gout or osteoporosis); metabolic or nutritive disorders or atthirties, gout or osteoporosis); metabolic or nutritive disorders or himson's contact or overty or with the protein and sorders of the kidney, liver, lung, because the capted of the colon or intention with the colon or col uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at the print pub/published\_pct\_sequences.

Sequence 353 AA;

ö 240 TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG 240 300 9 9 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS VFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVL 1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR 1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG 301 RPLQCWRPGVGVQGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353 ; 98.8%; Score 1787; DB 8; Length 353; 98.9%; Pred. No. 9.3e-175; ive 1; Mismatches 3; Indels Best Local Similarity 98.9 Matches 349; Conservative 61 61 121 181 181 241 301 Query Match 121 유 셤 g ò 셤 ⋧ g ò ò

ADO57997 standard; protein; 353 AA. RESULT 15 ADO57997

disease. The compositions have the following activities: analgeeic, antiarrhythmic, antiarteriosclerotic, antiasthmatic, antiacterial, antiarrhythmic, antiarteriosclerotic, antiasthmatic, antiacterial, antianter, activities antianter, carboraterive, dermatological, gynecological, neuroprotective, carboratorio, and virucide. The regulators of EDG5 are useful concropic, vasotropic, and virucide. The regulators of EDG5 are useful contropic, vasotropic, and virucide. The regulators of EDG5 are useful carboratorial diseases disorders of the peripheral and central nervous system, and respiratory diseases in a mammal. They are also useful for the regulation of EDG5 activity in a mammal having the disease.

Cardiovascular disease includes heart failure, myocardial infarction, cardiovascular disease includes heart failure, myocardial infarction, is chaemia, arrhythmias, and atherosclerosis. Examples of disorders of the gastricent erology system are dysphagia, Barrett's metaplasia, stress gastritis, gastric ulcers, and chronic pancreatitis. Examples of satrictis, and chronic pancreatitis. Examples of satrictis, dysmenorrhoea, and infartility. Disorders of the peripheral and central nervous system include Parkinson's disease, dementia, multiple sclerosis, etroke, and Alzheimer's disease. Respiratory diseases can be asthma or

The invention relates to a novel method for screening for therapeutic agents. The method comprises contacting a test compound with an endothelial differentiation sphingolipid G-protein-coupled receptor 5 compound, or determining EDGS polypeptide activity at a certain test compound concentration or in the absence of the test compound and at a different concentration of the test compound. The invention further comprises: diagnosing diseases such as a cardiovascular diseases, disorders of the gastroenterology system, reproductive diseases, disorders of the paripheral and central nervous system, and respiratory diseases in a mammal. The invention also comprises a pharmaceutical composition for the treatment of the diseases above comprising an EDGS polypeptide or which regulates the EDGS polypeptide

Disclosure; SEQ ID NO 2; 119pp; English.

endothelial differentiation sphingolipid; G-protein-coupled receptor 5; BGD5; cardiovascular disease; gastroenteroclogy system; reproductive; peripheral; central nervous system; respiratory; analgesic; antiarrhythmic; antiarteriosclerotic; antiasthmatic; antibacterial; central antianflammatory; antiparkinsonian; antiulcer; cardiant; cerebroprotective; dermatological; synecological; neuroprotective; nootropic; vasotropic; virucide; human. Screening for therapeutic agents, useful for treating e.g. respiratory disease, comprises contacting a test compound with endothelial differentiation sphingolipid G-protein-coupled receptor 5 polypeptide and Ή Summer 31-OCT-2003; 2003WO-EP012122. 13-NOV-2002; 2002EP-00025098. (FARB ) BAYER HEALTHCARE AG. Golz S, Brueggemeier U, WPI; 2004-449580/42. N-PSDB; ADO57996. detecting binding WO2004044587-A2 Homo sapiens. 27-MAY-2004. 

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chronic obstructive pulmonary disease. The nucleotide sequences encoding EDGS are useful as hybridization probes, in constructing oligomers for PCR, for chromosome and gene mapping, in the recombinant production of EDGS, in generating antisense DNA or RNA and in molecular biology techniques that have not yet been developed. EDGS polypeptides are useful for immunising a mammal to produce polyclonal antibodies and for diagnostic purposes. This sequence represents the human EDGS receptor protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VFIVCWLPAFSILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
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                                                                                                                                                                                                                                                                                                                                                            1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR 60
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                                                                                                                                                                                                                                            Query Match
98.8%; Score 1787; DB 8;
Best Local Similarity 98.9%; Pred. No. 9.3e-175;
Matches 349; Conservative 1; Mismatches 3;
                                                                                                                                                                                                       Sequence 353 AA;
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Search completed: December 4, 2005, 06:46:54 Job time : 131 secs

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281.714 Million cell updates/sec
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1 MGSLYSEYLNPWKVQEHYNY.....LERGMHMPTSPTFLEGNTVV 353
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1: /cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06 NEW FUB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26661 seqs, 4788334 residues
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Description         | Sequence 2, Appli | Sequence 4, Appli | Sequence 6, Appli | 26,               | β               | ď               | Seguence 6, Appli | Sequence 2, Appli | Sequence 44, Appl | Sequence 2, Appli | Sequence 118, App | Sequence 8, Appli | 1                 | Sequence 2, Appli | 93,               | Sequence 2, Appli | 4               | 1                 | Sequence 6, Appli | Sequence 66, Appl | Sequence 20, Appl | Sequence 2, Appli | 4,              | 'n              | Sequence 18, Appl |
|---------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-----------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-----------------|-------------------|
| ΔΙ                  | US-11-067-884-2   | US-11-067-884-4   | US-11-067-884-6   | US-10-851-667A-26 | US-10-992-577-8 | US-10-992-577-2 | US-10-992-577-6   | US-10-510-018-2   | US-10-992-577-44  | US-10-502-893-2   | US-10-980-388-118 | US-11-067-884-8   | US-10-980-388-112 | US-10-627-633-2   | US-10-821-234-934 | US-11-095-093-2   | US-10-627-633-4 | US-10-980-388-117 | US-10-627-633-6   | US-10-980-388-66  | US-11-068-686-20  | US-11-068-686-2   | US-11-068-686-4 | US-10-502-145-1 | US-10-131-826A-18 |
| 1 DB                | 7                 | 7                 | 7                 | 9                 | 9               | 9               | 9                 | 9                 | 9                 | 9                 | 9                 | 7                 | 9                 | 9                 | 9                 | 7                 | 9               | 9                 | 9                 | 9 /               | 7                 | 7                 | 5               | 9               | 9 /               |
| Length DB           | 364               | 351               | 353               | 360               | 430             | 432             | 420               | 522               | 417               | 440               | 342               | 419               | 208               | 415               | 485               | 313               | 405             | 34(               | 357               | 28,               | 35,               | 327               | 355             | 32(             | 34.               |
| *<br>Query<br>Match | 27.9              | 26.8              | 56.6              | 15.8              | 12.4            | 11.8            | 11.3              | 11.3              | 11.0              | 10:9              | 10.2              | 10.2              | 9.3               | 7.8               | 7.8               | 7.7               | 7.4             | 6.9               | 6.9               | 6.8               | 6.9               | 6.7               | 6.4             | 6.1             | 5.9               |
| Score               | 504               | 484               | 480.5             | 286               | 224.5           | 213.5           | 204.5             | 204.5             | 199.5             | 196               | 184               | 184               | 167.5             | 141               | 140               | 139               | 134             | 124.5             | 124.5             | 122               | 122               | 121               | 115             | 109.5           | 107               |
| Result<br>No.       | 1                 | 8                 | m                 | 4                 | ß               | 9               | 7                 | 8                 | 0                 | 10                | 11                | 12                | 13                | 14                | 15                | 16                | 17              | 18                | 19                | 20                | 21                | 22                | 23              | 24              | 25                |

| Sequence 119, App<br>Sequence 68, App<br>Sequence 61, App<br>Sequence 115, App<br>Sequence 63, App<br>Sequence 63, App<br>Sequence 64, App<br>Sequence 116, App<br>Sequence 2566, Ap<br>Sequence 201, App<br>Sequence 201, App<br>Sequence 201, App<br>Sequence 3106, App<br>Sequence 950, App<br>Sequence 950, App<br>Sequence 950, App<br>Sequence 950, App<br>Sequence 950, App<br>Sequence 950, App<br>Sequence 113, App<br>Sequence 118, App  | Sequence 2026, Ap  |
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| US-10-980-388-119 US-10-980-388-100 US-10-980-388-100 US-10-980-388-18 US-10-980-388-18 US-10-980-388-116 US-10-793-626-2566 US-10-793-626-3306 US-10-793-626- | US-10-793-626-2026 |
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### ALIGNMENTS

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APPLICANT: Virag, Tamas
APPLICANT: Virag, Tamas
APPLICANT: Nusser, Nora
TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTACONISTS AND METHODS OF
TITLE OF INVENTION: USE
FILE REFERENCE: 20609/305
CURRENT APPLICATION NUMBER: US/11/067,884
CURRENT APPLICATION NUMBER: US/0190,370
PRIOR PRILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 09/811,838
PRIOR PILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-19
PRIOR FILING NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.9%; Score 504; DB 7; Length 364;
34.3%; Pred. No. 6.4e-36;
tive 71; Mismatches 121; Indels 30; Gaps
          Sequence 2, Application US/11067884 Publication No. US20050261252A1 GENERAL INFORMATION:
                                                                    APPLICANT: Miller, Duane D. APPLICANT: Tigyi, Gabor APPLICANT: Tigyi, Gabor APPLICANT: Sardar, Vineet M. APPLICANT: Elrod, Don B. APPLICANT: Ku, Huiping APPLICANT: Wang, Dean APPLICANT: Liliom, Karoly APPLICANT: Fischer, David J.
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Fischer, David J.
Virag, Tamas
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Best Local Similarity 34.39
Matches 116; Conservative
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US-11-067-884-2
US-11-067-884-2
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120 LLVIAVERHMSIMRRMRVHSNLTKKRVTLLILLVWAIAIFMGAVPTLGMNCLCNISACSSL 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACSTV 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: LOS TITLE OF INVENTION: LOS TITLE OF INVENTION: USE TITLE OF INVENTION: USE TITLE OF INVENTION: USE TITLE OF INVENTION: USE CURRENT APPLICATION NUMBER: US/11/067,884

CURRENT APPLICATION NUMBER: 01/190,370

PRIOR FILING DATE: 2005-03-19

PRIOR FILING DATE: 2000-03-19

PRIOR FILING DATE: 2001-03-19

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver. 2.1
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306 ----WRPGVGVQGRRRGGTPGHHLLP 327
                                        315 LROSTŘESVHYTSSAQGGASTRIMLP 340
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US-10-851-667A-26
IS-10-851-667A-26
; Sequence 26, Application US/10851667A
; Publication No. US20050260608A1
; GENERAL INFORMATION:
                                                                                                                                                  ; Sequence 6, Application US/11067884; Publication No. US20050261252A1; GENERAL INFORMATION:
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Fischer, David J.
Virag, Tamas
Nusser, Nora
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Dalton, James T.
Sardar, Vineet M.
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Baker, Daniel L.
Wang, Dean
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Best Local Simi
Matches 101;
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                                        FSII-LLAIVALYVRIYCVVR----SSHADMAAPQ-----TLALLKTVTIVLGVFIVC 245
                                                                                                                            246 WLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVLRPLQC 305
                                                                                                                                                  271 WTPGLVLLLLDVCCP--QCDVLAYEKFPLLLAEFNSAMNPIIYSYRDKEMSATFRQILCC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 QLHTRMSNRRVVVVIVVIWTMAIVMGAIPSVGWNCICDIENCSNMAPLYSDSY-LVFWAI 212
                                                                                213 FNLVTFVVMVVLYAHİFGYVRQRTMRMSRHS--SGPRRNRDTMMSLLKTVVIVLGAFIIC 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 FSIILLAIVALYVRIYCVVRSSHADMA------APQTLALLKTVTIVLGVFIVCWLP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 AFSILLLD-YACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVLRPLQC-- 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 YNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARNSKFHSAMYLFLGNLAA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Liliom, Karoly
APPLICANT: Fischer, David J.
APPLICANT: Virag, Tamas
APPLICANT: Nusaer, Nora
TITLE OF INVENTION: LUSE
TITLE OF INVENTION: USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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35.9%; Pred. No. 3e-34;
ive 57; Mismatches 134; Indels
                                                                                                                                                                                                              306 WRPGVGCRRRGGTPGHHLLPLRSSSSLER----GMH 339
                                                                                                                                                                                                                                                      QR----SENPTGPTESSD----RSASSLNHTILAGVH 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 20609/305
CURRENT APPLICATION NUMBER: US/11/067,884
CURRENT FILING DATE: 2005-02-28
PRIOR APPLICATION NUMBER: 60/190,370
PRIOR PELING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 09/811,838
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                          ; Sequence 4, Application US/11067884; Publication No. US20050261252A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Miller, Duane D.
APPLICANT: Tigyi, Gabor
APPLICANT: Dalton, James T.
APPLICANT: Sardar, Vineet M.
APPLICANT: Elrod, Don B.
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Baker, Daniel L.
Wang, Dean
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Best Local Similarity 35.99
Matches 117; Conservative
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US-11-067-884-4
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APPLICANT: Jones, Kenneth A.
APPLICANT: Bonini, James A.
APPLICANT: Borowsky, Beth E.
APPLICANT: Craig, Douglas A.
TITLE OF INVENTION: DNA Brocding Mammalian Neuropeptide FF (NPFF) Receptors
TITLE OF INVENTION: And Uses Thereof
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SSANPIIYGYFNENFRRGFQAAFRARLCPRPSGSHKEAYSERPGGLLHRRVFVVVRPSDS 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 VAYALIFLLC---MVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDN 104
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.4%; Score 224.5; DB 6; Length 430; Best Local Similarity 24.3%; Pred. No. 2.6e-12; Matches 99; Conservative 59; Mismatches 128; Indels 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 SLLNPVIYTWRSRDLRR---EVLRPLQCWRP------------
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CURRENT APPLICATION NUMBER: US/L0/992,577
CURRENT FILING DATE: 2004-11-18
PRIOR APPLICATION NUMBER: US/09/538,036
PRIOR APPLICATION NUMBER: 09/405,558
PRIOR PLING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-02-24
PRIOR PLING DATE: 1999-02-22
PRIOR PLING DATE: 1999-02-22
PRIOR PLING DATE: 1999-02-22
PRIOR APPLICATION NUMBER: 09/161,113
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 430
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SEQ ID NO 2
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                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                 US-10-992-577-8
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                                                                                                                                                        APPLICANT: Shohami, Esther
APPLICANT: Shohami, Esther
APPLICANT: Shohami, Esther
APPLICANT: Mechoulam, Raphael
TITLE OF INVENTION: METHODS, KITS AND PHARMACEUTICAL COMPOSITIONS FOR DIAGNOSING,
TITLE OF INVENTION: DELAYING ONSET OF, PREVENTING AND/OR TREATING OSTEOPOROSIS
FILE REFERENCE: 28030
CURRENT APPLICATION NUMBER: US/10/851,667A
CURRENT PILING DATE: 2004-05-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.2
SEQ ID NO 26
LENGTH: 360
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Publication No. US20050260687A1

GENERAL INFORMATION:
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Bonini, James A.
APPLICANT: Borowsky, Beth E.
APPLICANT: Douglas A.
ITILE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
TITLE OF INVENTION: And Uses Thereof
FILE REFERENCE: 57155-D/JFW
CURRENT APPLICATION NUMBER: US/10/992,577

CURRENT FILING DATE: 2004-11-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 SASVFSLLAIAIRRHVAIAKVKLYGSDKSC----RMLLLIGASWLISLVLGGLPILGWNC 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 VTEIANGSKDGLDSNPMKDYMILSGPQKTAVAVLCTLLGLLGALBALFNVAVLYLILSSHXLR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 VQEHYNYTKETLETQETTSRQVAS----AFIVILCCAI----VVENLLVL-IAVARNSKF 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.8%; Score 286; DB 6; Length 360; Best Local Similarity 26.2%; Pred. No. 1.4e-17; Matches 89; Conservative 64; Mismatches 133; Indels
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LOCATION: (63) ...(63)
OTHER INFORMATION: Non-synonymous polymorphism: Gln or Arg
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de Vernejoul, Marie-Christine
Bab, Itai
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/405,558
PRIOR PILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: 09/255,368
PRIOR PILING DATE: 1999-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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                                                                                    APPLICANT:
APPLICANT:
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APPLICANT: Gerald, Christophe P.G.
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Gorald, Christophe P.G.
APPLICANT: Bonini, James A.
APPLICANT: Bonini, James A.
APPLICANT: Borowsky, Beth E.
APPLICANT: Borowsky, Beth E.
APPLICANT: Crast, Douglas A.
ITTLE OF INVENTION: And Uses Thereof
ITTLE OF INVENTION: And Uses Thereof
ITTLE OF INVENTION: And Uses 1910/992,577
CURRENT APPLICATION NUMBER: US/10/992,577
CURRENT FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: 09/405,588
PRIOR PELICATION NUMBER: 09/405,588
PRIOR APPLICATION NUMBER: 09/25,368
PRIOR FILING DATE: 1999-09-25
PRIOR FILING DATE: 1999-02-25
PRIOR FILING DATE: 1999-02-25
NUMBER OF SEQ ID NOS: 71
SCOTTWARE PATENTIN VOR: 71
                                     19;
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                                                                                                                                                             SDLLVGIFCMPTTLVDNLIT-------GWFFDNATCKMSGLVQGMSVSASVFTLV 135
                                                                                                                                                                                                                                   SDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAF------ITLSASVFSLL 124
                                                                                                                                                                                                            AIAIER----HVAIAKVKLYGSDKSCRMLLLIGASWLISLVL---GGLPILGWNCLGH- 175
                                                                                                                                                                                                                                                                                                                                                                                                                         259 -CPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRR---EVLRPLQCWRP----- 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------GVGVQGRRRGGTPGHHLLPLRSSSSLERG----- 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 AYSERPNRLLRRRVVVDVQPSDSGLPSESGPSSGVPGPGRLPLRNGRVAHQDGPGEGPGC 420
                                                                                                      28 TSLTFSSYYQHSSPVAAMFIAAYVLIFLLCMVGNTLVCFIVLKNRHMRTVTNMFILNLAV 87
                                                                                                                                                                                                                                                                                                      21 TKETLETQETTSRQVASAFI - - - VILCCAIVVENLLVLIAVARNSKFHSAMYLFLGNLAA
                                                                                                                                                                                                                                                                                                                                                   213 -----YCVVRSSHADMAAPQTLALLKTVTIVLGVFIVCWLPAFSILLL-DYA-----
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Query Match 11.8%; Score 213.5; DB 6; Length 432; Best Local Similarity 23.7%; Pred. No. 2.2e-11; Matches 102; Conservative 57; Mismatches 140; Indels 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89;
                                                                                                                                                                                                                                                                              176 -LEACSTVLPLYA------KHYVLCVVT-IFSIILLAIVALYVRI-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10992577
Publication No. US20050260687A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 23.4%
Matches 82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 NHMPLTIPAW 430
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Sequence 2, Application US/10510018
; Sequence 2, Application US.20050244896A1
; Publication No. US20050244896A1
; GENERAL INFORMATION:
; APPLICANT: GO1z, Stefan
; APPLICANT: Weingarten, Bernhard
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
; TITLE OF INVENTION: Diagnostics and Therapeutic for Diseases Associated with
; TITLE OF INVENTION: Diagnostics and Therapeutic for Diseases Associated with
; TITLE OF INVENTION: Diagnostics and Therapeutic for Diseases Associated with
; TITLE OF INVENTION: Diagnostics and Therapeutic for Diseases Associated with
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
; TURENT APPLICATION NUMBER: US/10/510,018
; CURRENT FILING DATE: 2004-10-01
; PRIOR FILING DATE: 2003-03-21
; PRIOR FILING DATE: 2003-04-02
; PRIOR PLICATION NUMBER: EP 02007270.8
; PRIOR SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
ILENTH: 522
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                                                                                                                                                                                                                                                           116 LSASVESLLAIAIAIERHVAIA---KVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNC 172
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129 VAASVFILVAIAVDRFQCVVYPFKPKL-TIKTAFVIIMI--IWVLAITI------ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                         231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 VALYVRIYCVVRSSHADMAAPQT------LALLKTVTIVLGVFIVCWLPAF 250
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63
                                                         18 NVNDTKHHLYSDINITYVNYYLHQPQVAAIFIISYFLIFFLC--MMGNTVVCFIVMRNKH 75
                                                                                                                                                                      64 FHSAMYLFLGNLAASDLLAGVAFVANTLLS-----GSVTLRLTPVQWFAREGSAFIT
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231 VAASVFTLVAIAVDRFQCVVYPFKPKL--TIKTAFVIIMI--IWVLAITI------
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10 NPNKVQEH-----YNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARNSK
                                                                                                                             64 FHSAMYLFLGNLAASDLLAGVAFVANTLLS-----GSVTLRLTPVQWFAREGSAFIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 SILLL-DYA-CPVHSCPILYKAHYXFA--VSTLNSLLNPVIYTWRSRDLRR 297
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                                                                                                                                                                                                                                                                                                                                                                                           LGHLEACSTVLPLYAKHYV------
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US-10-510-018-2
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                                                                                                                                             general information no. Uszucbue8/Al

general information no. Uszucbue8/Al

general information.

APPLICANT: Gerald, Christophe P.G.

APPLICANT: Bornois, Menneth A.

APPLICANT: Bornois, Meth B.

APPLICANT: Craig, Douglas A.

ITLE OF INVENTION: DAM Encoding Mammalian Neuropeptide FF (NPFF) Receptors

TITLE OF INVENTION: And Uses Thereof

FILE REFERENCE: 57155-D/JPM

CURRENT APPLICATION NUMBER: US/10/992,577

CURRENT APPLICATION NUMBER: US/09/538,036

PRIOR APPLICATION NUMBER: 09/405,558

PRIOR PILING DATE: 1999-09-24

PRIOR PILING DATE: 1999-02-24

PRIOR APPLICATION NUMBER: 09/161,113

PRIOR PILING DATE: 1999-02-25

NUMBER OF SEQ ID NOS: 71

SEQ ID NO 44

LENGTH 417
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297
                    394 TLMMLSDYADLSPNELQIINIYIYPPAHWLAFGNSSVNPIIYGFFNENFRR 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 417;
251 SILLL-DYA-CPVHSCPILYKAHYXFA--VSTLNSLLNPVIYTWRSRDLRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ::| | :| | RN-----LDINTSGLL---VHEPAS 382
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                                                                                                      US-10-992-577-44
; Sequence 44, Application US/10992577
; Publication No. US20050260687A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Rattus norvegicus
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Best Local Similarity 22.74
Matches 88; Conservative
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; Sequence 2, Application US/10502893

US-10-502-893-2

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Sequence 118, Application US/10980388
Publication No. US20050255490A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Parodi, Luis A.
APPLICANT: Hebsch, Ronald R.
APPLICANT: Lind, Peter APPLICANT: Ruff, Valerie
APPLICANT: Ruff, Valerie
APPLICANT: Ruff, Valerie
APPLICANT: Wood, Lind B.
APPLICANT: Wood, Lind B.
APPLICANT: Wood, Lind M.
APPLICANT: Wood, Lind S.
APPLICANT: Wood Lind S.
                                                                                                                                                               and Therapeutics for Diseases Associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 -VANTLLSGSVTLRLTPVQWFAREGSAFITLSASVFSLLAIAIERHVAIAKVKLYGSDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 VASAFIVILCCAIVVENLLVLI----AVARNSKFHSAMYLFLGNLAASDLLAGVAF---
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25.5%; Pred. No. 6.7e-10;
ative 51; Mismatches 135;
                                      APPLICANT: Bayer HealthCare AG
APPLICANT: Golz, Stefan
APPLICANT: Bruggemeier, Ulf
APPLICANT: Geerts, Andreas
TITLE OF INVENTION: Diagnostics and Therapeu:
TITLE OF INVENTION: Human 5HT6 Receptor
FILE REPERENCE: LeA 35 827
FILE REPERENCE: LeA 35 827
CURRENT APPLICATION NUMBER: US/10/502,893
CURRENT FILING DATE: 2004-07-27
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2002-02-01
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SOFTWARE: Patentin version 3.2
SEQ ID NO
LENCTH: 440
US20050255529A1
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Best Local Similarity
Matches 96; Conserv
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US-10-980-388-118
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                   LENGTH: 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: || :: |: || :: || 212 MILLYSKIFLIAKQQAIKIETTSSKVESSSESYKIRVAKRERKAAKTLGVTVLAFVISWL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 VVENLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFA 107
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APPLICANT: Sardar, Vineet M.
APPLICANT: Sardar, Vineet M.
APPLICANT: Brod, Don B.
APPLICANT: Wing Dan B.
APPLICANT: Wang, Dean
APPLICANT: Wang, Dean
APPLICANT: Fischer, David J.
APPLICANT: Virag, Tamas
APPLICANT: Norag, Tamas
APPLICANT: Norag, Tamas
APPLICANT: Norag, Tamas
APPLICANT: Norag, Tamas
APPLICANT: Norager, Nora
TITLE OF INVENTION: USR
PRIOR APPLICATION NUMBER: US/09/791,932
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2000-02-23
PRIOR PLICATION NUMBER: 60/184,305
PRIOR PLICATION NUMBER: 60/184,304
PRIOR APPLICATION NUMBER: 60/184,304
PRIOR APPLICATION NUMBER: 60/184,303
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,397
PRIOR PILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,247
PRIOR PLILING DATE: 2000-02-23
PRIOR PLILING DATE: 2000-02-23
PRIOR PLILING DATE: 2000-03-13
PRIOR PLILING DATE: 2000-03-11
PRIOR APPLICATION NUMBER: 60/217,369
PRIOR APPLICATION NUMBER: 60/217,370
PRIOR APPLICATION NUMBER: 60/219,492
PRIOR PLILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/218,492
PRIOR APPLICATION NUMBER: 60/218,492
PRIOR PLILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/218,492
PRIOR PLILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/218,492
PRIOR PLILING DATE: 2000-07-11
PRIOR PLILING DATE: 2000-07-11
PRIOR PLILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/218,492
PRIOR PLILING DATE: 2000-07-11
PRIOR PLILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/218,492
PRIOR PLILING DATE: 2000-07-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 342;
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1 Similarity 22.4%; Pred. No. 5.2e-09;
64; Conservative 53; Mismatches 103; Indels
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Publication No. US20050261252A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 64; Conserv
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US-11-067-884-8
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LENGTH: 342
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APPLICANT: Parcel, Luis A.
APPLICANT: Hiebsch, Ronald R.
APPLICANT: Hiebsch, Ronald R.
APPLICANT: Hiebsch, Ronald R.
APPLICANT: Hiebsch, Ronald R.
APPLICANT: Lind, Peter E.
APPLICANT: Raytes, Paul S.
APPLICANT: Ruff, Valerie
APPLICANT: Wood, Linda S.
TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl TILE REFRENCE: 00325.US1
CURRENT APPLICATION NUMBER: US/10/980,388
CURRENT FILING DATE: 2004-11-02
PRIOR APPLICATION NUMBER: 60/184,305
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,305
PRIOR FILING DATE: 2000-02-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 SFFIPFLVILYSFMGILNTLRHNALRIHSYPEGICLSQASKLGLMSLQRPFQMSIDMGFK 309
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CURRENT APPLICATION NUMBER: US/11/067,884
CURRENT FILING DATE: 2005-02-28
PRIOR APPLICATION NUMBER: 60/190,370
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 8
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APPLICANT: Parodi, Luis A.
APPLICANT: Hiebsch, Ronald R.
APPLICANT: Lind, Peter
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55 LIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLLS----
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Best Local Similarity 21.9%;
Matches 62; Conservative 5:
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ORGANISM: Homo sapiens
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US-10-821-234-934
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          PRIOR FILING DATE: 2000-02-23
PRIOR PILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,247
PRIOR APPLICATION NUMBER: 60/188,880
PRIOR FILING DATE: 2000-03-13
PRIOR FILING DATE: 2000-07-11
PRIOR PILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                          9.3%; Score 167.5; DB 6; Length 508;
44.7%; Pred. No. 2e-07;
ve 48; Mismatches 84; Indels 17
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Best Local Similarity 24.5%; Pred. No. 2.7e-05;
Matches 87; Conservative 54; Mismatches 128;
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APPLICANT: Charles, Andrew David
APPLICANT: Brennand, John Charles
APPLICANT: Hart, Kevin Anthony
IILE OF INVENTION: Novel Compound
FILE REPERENCE: 1991-221
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: 09/722,342
PRIOR FILING DATE: 2000-11-28
PRIOR PILING DATE: 1999-12-17
PRIOR PILING DATE: 1999-12-17
SEQ ID NO 2: 6
SOFTWARE: Patentin version 3.2
SEQ ID NO 2: 6
SEQ ID NO 2: 6
SEQ ID NO 2: 6
SEQ ID NO 3.2
APPLICATION NUMBER: 60/184,397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 VMIACYSVVFCAARROHA 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.78;
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Matches 49; Conservative
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US-10-627-633-2
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US-10-627-633-2
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Sequence 934, Application US/10821234
; Sequence 934, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
    APPLICANT: Labat, Ivan
; APPLICANT: Application is Susan
; APPLICANT: Tang, Y. Tom
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; TITLE OF INVENTION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR APPLICATION NUMBER: 2003-04-07
; RIOR APPLICATION STATE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 NLLVLIAVARNSKFHSAMYLFLGNLAASDLL--AGVAFVANTLLSGSVTLRLTPVQW-FA 107
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                                                                                                                                                                                                                                                                                                                                    194 FVTPVLFFYGSNWDSH---CNYFLPSSWEGTAYTVIHFLVGFVIPSVLILFYQKVIKXI 250
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                                                                                                                145 -----QYLTPGVQIYVLLSICIDRFYTIVYPLSFKVSREKAKK------MIAASWIFDAG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 -RIYCVVRSSHADM-AAPQT-LALLKTVTIVLGVFIVCWLPAFSILLL-----DYACPV 261
                                                                                                                                                                                                                                                           160 LVLGGLPILGWNCLGHLEACSTVLP-----LYAKHYVLCVVTIFSIILLAI----VALYV
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241 VFIVCWLPAFSILLIDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVL 300
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1806
1 MGSLYSEYLNPNKVQEHYNY......LERGMHMPTSPTFLEGNTVV 353
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-084-507B-22

US-09-842-316-8

US-09-971-228-9

US-10-224-504-508

US-10-224-567A-508

US-10-228-9

US-10-21-828-8

US-10-21-828-8

US-10-421-828-8

US-10-41-828-8

US-10-41-828-8

US-10-41-828-8

US-10-41-828-4

US-09-904-09-37

US-09-904-09-37

US-09-764-886-74

US-09-764-886-74

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US-10-633-438-65
US-10-901-772-65
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Sequence 2, Application US/09771063
Fatent NO. US20010034331A1
GENERAL INFORMATION:
APPLICANT: Derk J. Bergama
APPLICANT: Nabil Elshourbagy
APPLICANT: Pamela Lane
APPLICANT: Aiactong Li
APPLICANT: Ping Teui
TITLE OF INVENTION: EDG FAMILY GENE, HUMAN H218
FILE REFERENCE: GF-0431-C.
CURRENT APPLICATION NUMBER: US/09/771,063
CURRENT PILING DATE: 2001-01-26
FRIOR APPLICATION NUMBER: 09/150,650
FRIOR APPLICATION NUMBER: 60/082,776
FRIOR FILING DATE: 1998-09-03
FRIOR FILING DATE: 1998-04-23
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
US-11-026-435-8
US-09-971-228-13
US-09-871-228-5
US-09-861-455-2
US-09-759-514-2
US-10-099-11
US-10-225-567A-237
US-10-225-567A-237
US-10-295-160-72
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0; Mismatches
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Best Local Similarity 99.7
Matches 352, Conservative
  CRGANISM: HOMO SAPIENS US-09-771-063-2
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                                                                                                                                                                               APPLICANT: KAMBO, RAJENDER
APPLICANT: KAMBO, RAJENDER
APPLICANT: PEFERS, DIANA
APPLICANT: PEFERS, DIANA
APPLICANT: PEFERS, DIANA
APPLICANT: VYAS, TEJAL B.
APPLICANT: GUTTA, ASHWANI K.
TILLE OF INVENTION: AN ISOLATED HUMAN EDG-4 RECEPTOR
FILE REFERENCE: 108074-00023
CURRENT APPLICATION NUMBER: US,10/084,507B
CURRENT FILING DATE: 2002-08-12,995
PRIOR APPLICATION NUMBER: 06/090,610
PRIOR PELING DATE: 1998-11-25
PRIOR PILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: 60/090,610
PRIOR APPLICATION NUMBER: 60/090,610
PRIOR APPLICATION NUMBER: 60/070,185
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1997-12-30
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 17
LENGTH: 353
                                                                                                                            Sequence 17, Application US/10084507B Publication No. US20030054452A1 GENERAL INFORMATION:
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US-10-084-5078-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MOD RES
LOCATION: (273)
                                                                                                                US-10-084-507B-17
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US-09-731-030A-19 ; Sequence 19, Application US/09731030A

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MUNROE, Abhwani K.
APPLICANT: ZASTAMNY, Roman L.
TITLE OP INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
TITLE OP INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
TITLE REFERENCE: 8074-0015
CURRENT APPLICATION NUMBER: US/09/731,030A
CURRENT FILING DATE: 1998-12-29
PRIOR APPLICATION NUMBER: 60/070,184
PRIOR APPLICATION NUMBER: 60/070,184
PRIOR PILING DATE: 1997-12-30
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 19
SEQ ID NO 19
LENGTH: 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.8%; Score 1803; DB 3;
Best Local Similarity 99.4%; Pred. No. 3.4e-156;
Matches 351; Conservative 1; Mismatches 1;
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APPLICANT: FETERS, DIANA
APPLICANT: PETERS, DIANA
APPLICANT: PETERS, DIANA
APPLICANT: WYAS, TEJAL B.
APPLICANT: GUFFA, AEHWANI K.
TITLE OF INVENTION: AN ISOLATED HUMAN EDG-4 REC
TITLE OF INVENTION: AN ISOLATED HUMAN EDG-4 REC
CURRENT APPLICANTION NUMBER: US/10/084,507B
CURRENT PELLING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/222,995
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-36
PRIOR FILING DATE: 1998-11-25
PRIOR FILING DATE: 1998-10-36
PRIOR FILING DATE: 1998-10-36
PRIOR FILING DATE: 1998-10-36
PRIOR FILING DATE: 1998-10-36
PRIOR FILING DATE: 1998-10-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Unknown
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APPLICANT: Chu, Peter
APPLICANT: Chu, Peter
APPLICANT: Chu, Peter
APPLICANT: Li, Congfen
APPLICANT: Li, Congfen
APPLICANT: Shao, Hacran
APPLICANT: Jiang, Yingping
APPLICANT: Migel Pharmaceuticals, Incorporated
APPLICANT: Nigel Pharmaceuticals, Incorporated
APPLICANT: Nigel Pharmaceuticals, Incorporated
APPLICANT: Nighting
APPLICANT: Sigel Pharmaceuticals, Incorporated
APPLICANT: 201044-000310US
CURRENT APPLICATION NUMBER: US/09/971,228
CURRENT APPLICATION NUMBER: US 60/284,763
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 15.
SOFTWARE: PatentIn Ver. 2.1
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     181 TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
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Patent No. US20020155512A1
GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Homo sapiens
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Matches 350; Conserv
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APPLICANT: KOSTENSIS, Eva

APPLICANT: GASSENHUBER, Johann

TITLE OF INVENTION: EDG8 RECEPTOR, ITS PREPARATION AND USE

FILE REFERENCE: 38065-147

CURRENT APPLICATION NUMBER: US/09/842,316

CURRENT APPLICATION NUMBER: EP 116589.3

PRIOR PILING DATE: 2001-04-26

PRIOR PILING DATE: 2000-08-01

PRIOR PILING DATE: 2000-04-26

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PACENTIN VERSION 3.1

SEQ ID NO 8

LENGTH: 353
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                                                                                                                                                                                        Indels
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                                                                                                                                                  Score 1803; DB 4;
Pred. No. 3.4e-156;
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larity 99.2%; Pred. No. 9.8e-155;
Conservative 0; Mismatches 3;
                                                                                                                                                                                      1; Mismatches
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Patent No. US20020099191A1
                                                                                                                                                  Query Match
Best Local Similarity 99.4%;
Matches 351; Conservative 1
SOFTWARE: Patentin Ver. 2; SEQ ID NO 22; LENGTH: 353
                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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Matches 350; Conserv
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US-09-842-316-8
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98.9%; Score 1787; DB 4; Length 353;
Best Local Similarity 99.2%; Pred. No. 9.8e-155;
Matches 350; Conservative 0; Mismatches 3; Indels
    Length 353
                                              Indels
Score 1787; DB 4;
Pred. No. 9.8e-155;
0; Mismatches 3;
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APPLICANT: Huang, Ling Yan
APPLICANT: Borowsky, Beth E.
APPLICANT: Salon, John A.
APPLICANT: Salon, John A.
APPLICANT: Majorn, Amy
TITLE OF INVENTION: NAME SOLON, Raisa
TITLE OF INVENTION: DNA Encoding Edg7 Receptor
FILE REFERENCE: 58230-a
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: US/09/356,315
PRIOR APPLICATION NUMBER: 09/253,998
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0 - beta
SEQ ID NO 19
LENGTH: 353
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    98.9%;
99.2%;
  Query Match
Best Local Similarity 99.21
Matches 350; Conservative
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US-10-228-762-19
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Publication No. US20030113798A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Rough, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A

PRIOR PILING DATE: 2001-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
LENGTH: 353
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                                                              Sequence 33, Application US/09904099

Publication No. US20030119092A1

GENERAL INFORMATION:

APPLICANT: Shankar. Geetha

APPLICANT: Spencer, Juliet V

TITLE OF INVENTION: CHIMERIC G PROTEIN COUPLED RECEPTORS

FILE REFERENCE: 10602-013-999

CURRENT APPLICATION NUMBER: US/09/904,099

CURRENT FILING DATE: 2001-07-11

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin version 3.1

SEQ ID NO 33
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99.2%; Pred. No. 9.8e-155;
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Best Local Similarity 99.2'
Matches 350; Conservative
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; ORGANISM: Homo sapiens
US-09-904-099-33
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ORGANISM: Homo sapiens
US-10-225-567A-508
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US-10-225-567A-508
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CURRENT APPLICATION NUMBER: US/10/421,828

CURRENT FILING DATE: 2003-05-08

PRIOR PILING DATE: 2000-08-01

PRIOR FILING DATE: 2000-08-01

PRIOR FILING DATE: 2000-08-01

PRIOR FILING DATE: 2000-04-26

NUMBER: PP 108858.2

NUMBER: PP 108958.2

SEQ ID NOS: 9

SOFTWARE: PLENTING DATE: 2000-04-26

NUMBER: PP 108958.2
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 353;
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APPLICANT: LI, JUNG
APPLICANT: LI, JUNG
APPLICANT: SIN, WIDN CHEX
APPLICANT: SIN, WIDN CHEX
TITLE OF INVENTION: AMPLIFIED GENES INVOLVED IN CANCER
FILE REFERENCE: 38002-062
CURRENT APPLICATION NUMBER: US/10/715,117
CURRENT FILING DATE: 2003-11-18
PRIOR FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 60/427,202
PRIOR APPLICATION NUMBER: 60/427,404
PRIOR APPLICATION NUMBER: 60/434,434
PRIOR PELING DATE: 2002-11-19
SROFTWARE: PATCHIN VET: 3.2
SOFTWARE: PATCHIN VET: 3.2
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Pred. No. 9.8e-155;
0; Mismatches 3;
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Pred. No. 9.8e-155;
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99.2%;
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TYPE: PRT
CRGANISM: Homo sapiens
US-10-715-117-7
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ORGANISM: Homo sapiens
US-10-421-828-8
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Best Local Similarity
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Best Local Similarity
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US-10-715-117-7
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APPLICANT: SIELGER, Karl-Ernet
APPLICANT: SIELGER, Martina
APPLICANT: JACOBS, Martina
APPLICANT: MACE, Sandrine
APPLICANT: MEEV Jean-Francois
APPLICANT: MACE, Sandrine
APPLICANT: DEBLEUZE, Jean-Francois
TITLE OF INVENTION: ASSOCIATION OF EDGS POLYMORPHISM WITH TYPE II DIABETES MELLITUS,
TITLE OF INVENTION: VENOUS THROMBOSIS OR PULMONARY EMBOLISM AND THE USE THEREOF
FILE REFERENCE: DEAVISOR/0019 US NP
CURRENT APPLICATION UMBER: US/10/393,870
CURRENT PILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 4
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/10393870
Publication No. US20030219808A1
GENERAL INFORMATION:
APPLICANT: KOZIAN, Detlef
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SEQ ID NO 3
LENGTH: 353
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US-10-393-870-3
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US-10-421-828-8
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121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNWLGHLEACS
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Pred. No. 2.3e-154;
0; Mismatches 4; Indels
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Sequence 4, Application US/09771063
Sequence 4, Application US/09771063
Sequence 4, Application US/09771063
Septeman No. US/201003431A1
Septeman Nabil Elshourbagy
APPLICANT: Pamela Lane
CURRENT: Ping Tsui
TITLE OF INVERTION: EDG FAMILY GENE, HUMAN H210;
CURRENT FILING DATE: 201-01-26
CURRENT FILING DATE: 1998-09-03
FRIOR APPLICATION NUMBER: 09/150,650
FRIOR APPLICATION NUMBER: 09/150,650
FRIOR APPLICATION NUMBER: 09/150,650
FRIOR FILING DATE: 1998-04-23
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 353
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Publication No. US20030054452A1
PENERAL INPORMATION:
APPLICANT: MUNROE, DONALD G.
APPLICANT: KAMBOJ, RAJENDER
APPLICANT: PETERS, DIANA
APPLICANT: KOOSHESH, FATEMEH
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Best Local Similarity 98.9%;
Matches 349; Conservative 0
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US-10-084-507B-21
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US-09-771-063-4
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99.2%; Pred. No. 9.8e-155;
iive 0; Mismatches 3;
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US-10-498-46

Sequence 46, Application US/10498848

Publication No. US20050153289A1

GENERAL INFORMATION:

APPLICANT: Takeda Chemical Industries, Ltd.

TITLE OF INVENTION Method of Analyzing Gene Exp.

FILE REFERENCE: P02-0155PCT

CURRENT APPLICATION NUMBER: US/10/498,848

CURRENT FILING DATE: 2004-06-14

PRIOR FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: JP 2002-45104

PRIOR APPLICATION NUMBER: JP 2002-45104

PRIOR APPLICATION NUMBER: JP 2002-140111

PRIOR APPLICATION NUMBER: JP 2002-140111

PRIOR FILING DATE: 2002-05-15

PRIOR FILING DATE: 2002-11-12

SEQ ID NOS: 77

LEMCHALL SEQ ID NOS: 77
      0; Mismatches
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Matches 350; Conservative
      350; Conservative
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APPLICANT: VYAS, TEJAL B.
APPLICANT: GUPTA, ASHWANI K.
ITTLE OF INVENTION: AN ISOLATED HUMAN EDG-4 RECEPTOR FILE REFERENCE: 1080/14-00023
CURRENT APPLICATION NUMBER: US/10/084,507B
CURRENT PILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/222,995
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 60/109,885
PRIOR FILING DATE: 1998-11-25
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1997-12-30
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VEY: 2.1
LENGTH: 352
LENGTH: 352
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Search completed: December 4, 2005, 06:42:08 Job time: 117.5 secs



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Sequence 4, Appli
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1 MGSLYSEYINPNKVQEHYNY......LERGMHMPTSPTFLEGNTVV 353
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
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(c) 1993 - 2005 Compugen Ltd
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US-09-582-200A-12

US-09-71-030A-19

US-09-74-752D-3

US-08-196-989B-2

US-08-196-98B-2

US-08-196-98B-2

US-08-196-98B-2

US-09-169-205D-24

US-09-169-205D-24

US-09-262-04-12

US-09-262-04-12

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US-08-845-566-3
US-08-467-948A-28
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US-08-467-947A-28
US-09-731-030A-17
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Maximum Match 100%
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Sequence 2, Application US/09582200A

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Sequence 2, Application US/09582200A

Sequence 2, Application US/09582200A

GENERAL INFORMATION:

APPLICANT: Kamboj, Rajender

APPLICANT: Kamboj, Rajender

APPLICANT: Kooshesh, Fatemeh

APPLICANT: Was, Tejal B.

APPLICANT: Uyas, Tejal B.

APPLICANT: Uyas, Tejal B.

APPLICANT: Uyas, Tejal B.

APPLICANT: Uyas, Usono 00002

CURRENT APPLICANTON NUMBER: US/09/582,200A

FILE REFERENCE: 108074-00002

CURRENT APPLICATION NUMBER: US/02/22,995

PRIOR PILING DATE: 1998-11-25

PRIOR PILING DATE: 1998-11-25

PRIOR FILING DATE: 1998-11-25

PRIOR FILING DATE: 1998-11-25

PRIOR FILING DATE: 1998-11-25

PRIOR FILING DATE: 1998-12-30

PRIOR FILING DATE: 1998-11-25

PRIOR FILING DATE: 1998-12-30

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PRIOR FILING DATE: 1998-14-33

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Sequence 2, Appli
Sequence 23, Appl
Sequence 1, Appli
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100.0%; Pred. No. 2.6e-146;
tive 0; Mismatches 0; Indels
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US-09-731-030A-11
US-09-731-030A-11
US-09-731-030A-13
US-09-731-030A-13
US-09-731-030A-13
US-09-169-2050-20
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US-09-169-2050-20
US-09-169-2050-23
US-09-731-030A-15
US-09-731-030A-15
US-09-169-2050-23
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 353; Conserv
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US-09-082-088-2

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Sequence

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Sequence Sequence

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Referse, Donald G.
APPLICANT: Referse, Datana
APPLICANT: Rooshesh, Ratemeh
APPLICANT: Wooshesh, Ratemeh
APPLICANT: WOOSHES: Wooloo?
CURRENT FILING DATE: 1998-12-30
FRIOR APPLICATION NUMBER: GO/109, 885
FRIOR APPLICATION NUMBER: GO/00, 185
FRIOR FILING DATE: 1998-10-25
FRIOR FILING DATE: 1998-04-03
FRIOR FILING DATE: 1999-12-30
FRIOR FILING DATE: 1999-12-30
FRIOR FILING DATE: 1999-12-30
FRIOR FILING DATE: 1999-12-30
FRIOR FILING DATE: 1999-13-30
FRIOR APPLICATION NUMBER: GO/070, 185
FRIOR FILING DATE: 1999-12-30
FRIOR FILING DATE: 1997-12-30
FRIOR FILING DATE: 1
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                                    181 TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG 240
                                                                                                                                      241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
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241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
      TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; LCCATION: (273)..(273)
; OTHER INFORMATION: "Xaa" represents any amino acid
US-09-582-200A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09582200A
Patent No. 6482609
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APPLICANT: Munroe, Donald G.
APPLICANT: Munroe, Day, Rajender
APPLICANT: Seeken, Diana
APPLICANT: Acabod, Rajender
APPLICANT: Gupta. Ashwani
TITLE OF INVENTION: IDENTIFICATION OF LYSCLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
FILE REFERENCE: 108074-00002
CURRENT APPLICATION NUMBER: US/09/582,200A
CURRENT APPLICATION NUMBER: 09/222,995
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-11-25
PRIOR PELLORICATION NUMBER: 60/080,610
PRIOR PELLOR DATE: 1998-11-25
PRIOR PELLOR DATE: 1998-12-30
PRIOR PELLOR DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
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100.0%; Pred. No. 2.6e-146;
iive 0; Mismatches 0;
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LOCATION: (272)..(274)
OCHER INFORMATION: Unknown Xaa = Leu or Pro
FEATURE:
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i LOCATION: (273].
i CTER INFORMATION: Unknown Xaa = Leu or Pro
US-09-582-200A-5
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Patent No. 6482609
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Best Local Similarity 100.0
Matches 353, Conservative
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                                                                                                                          Sequence 4, Application US/09582200A

Sequence 4, Application US/09582200A

Patent No. 6482609

GENERAL INFORMATION

APPLICANT: Munroe, Donald G.

APPLICANT: Remboj, Rajender

APPLICANT: Peters, Diana

APPLICANT: Gupta, Ashwani

TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE

FILE REFERENCE: 108074-00002

CURRENT APPLICATION NUMBER: US/09/582,200A

CURRENT FILING DATE: 1998-12-30

CURRENT FILING DATE: 1998-12-30

PRIOR FILING DATE: 1998-12-30

PRIOR FILING DATE: 1998-12-30

PRIOR FILING DATE: 1998-12-30

PRIOR PILING DATE: 1998-04-03

PRIOR FILING DATE: 1998-04-03

PRIOR FILING DATE: 1998-12-30

PRIOR FILING DATE: 1998-04-03

PRIOR FILING DATE: 1998-12-30

PRIOR FILING DATE: 1998-12-30

PRIOR PELING DATE: 1998-04-03

PRIOR PELING DATE: 1998-12-30

NUMBER OF SEQ ID NOS: 14

SOUTHWARE OF SEQ ID NOS: 14
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Pred. No. 3.1e-146;
1; Mismatches 1;
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Best Local Similarity 99.4%;
Matches 351; Conservative
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US-09-582-200A-6
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Sequence 6, Application US/09582200A Patent No. 6482609 GENERAL INFORMATION:

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APPLICANT: Peters, Diana
APPLICANT: Roshesh, Fatemeh
APPLICANT: Koshesh, Fatemeh
APPLICANT: Koshesh, Fatemeh
APPLICANT: Gupta, Ashwani
FILE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
FILE REFERENCE: 108074-00002.
FILE REFERENCE: 108074-00002.
CURRENT APPLICATION NUMBER: US/09/582,200A
CURRENT PILING DATE: 1998-12-30
FRIOR FILING DATE: 1998-12-30
FRIOR FILING DATE: 1998-11-25
FRIOR PRICK TOWNER: 60/080,610
FRIOR FILING DATE: 1998-04-03
FRIOR FILING DATE: 1998-04-03
FRIOR FILING DATE: 1998-11-25
FRIOR FILING DATE: 1998-04-03
FRIOR FILING DATE: 1998-04-03
FRIOR FILING DATE: 1997-12-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VERSION 3.1
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TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY R-
FILE REFERENCE: 108074-00002
CURRENT APPLICATION NUMBER: US/09/582,200A
CURRENT FILING DATE: 2000-07-28
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Pred. No. 3.1e-146;
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1; Mismatches
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Patent No. 6482609
GENERAL INFORMATION:
APPLICANT: Munroe, Donald G.
APPLICANT: Ramboj, Rajender
APPLICANT: Peters, Diana
APPLICANT: Kooshesh, Fatemeh
APPLICANT: Yyas, Tejal B.
APPLICANT: Gupta, Ashwani
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Best Local Similarity 99.4
Matches 351; Conservative
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US-09-582-200A-6
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181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG 240
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APPLICANT: An, Songalu
TITLE OF INVENTION: Shaingolipids and TITLE OF INVENTION: Shaingolipids and TITLE OF INVENTION: Shaingolipids and Nucleic Acids Encoding the Same FILE REFERENCE: A-67501/DDB/TAL; CURRENT APPLICATION NUMBER: US/09/274,752D
CURRENT FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                               61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV
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Pred. No. 1.5e-142;
0; Mismatches 6;
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Best Local Similarity
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US-09-274-752D-3
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US-09-731-030A-19
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Pred. No. 3.1e-146;
1; Mismatches 1;
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99.4%; Pred. No. 3.1e-146;
iive 1; Mismatches 1;
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Fatent No. 6566096
GENERAL INFORMATION:
APPLICANT: GUPTA, Ashwani K.
APPLICANT: GUPTA, Ashwani K.
TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOM:
FILE REFERENCE: 8074-0015
CURRENT APPLICATION NUMBER: US/09/731,030A
CURRENT FILING DATE: 1998-12-29
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: PCT/CA98/01195
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-11-35
PRIOR PLILNG DATE: 1998-11-25
PRIOR PRILNG DATE: 1998-11-25
PRIOR PRILNG DATE: 1998-12-30
PRIOR FILING DATE: 1997-12-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PALENTIN VUMBER: 60/70,185
SEQ ID NO 12
SEQ ID NO 12
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PRIOR FILING DATE: 1997-12-30
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 353
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Matches 351; Conservative
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Best Local Similarity
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ORGANISM: Unknown
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US-09-731-030A-19
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89.8%; Pred. No. 4.6e-131;
iive 13; Mismatches 22; Indels 1;
                                                                                                  GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
TITLE OF INVENTION: G-Protein Coupled Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,989B
FILING DATE: 15-FEB-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                    ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REGISTRATION NUMBER: MAC-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                 Sequence 2, Application US/08196989B Patent No. 5585476
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                      Floppy disk
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 89.87
Matches 317; Conservative
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COMPUTER READABLE FORM:
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241 VFIICWLPAFSILLLDSTCPVRACPVLYKAHYPFAFATLNSLLNPVIYTWRSRDLRREVL 300
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Sequence 2, Application US/08760936
Patent No. 5856443
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
TITLE OF INVENTION: G-Protein Coupled Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE 314wanchik, Lloyd & Saliwanchik, STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.0%; Score 1625.5; DB 1; Length
89.8%; Pred. No. 4.6e-131;
tive 13; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                        CUDNIKY: 05

CUDNIKY: 05

CUDNIKY: 05

CUDNIKY: 05

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPTITE: 1BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,936

FILING DATE: December 6, 1996

CLASSIFICATION: 536

ATTORNEY, AGENT INFORMATION:
NAME: Pace, Doran R.
REFERENCE/DOCKET NUMBER: 38,261

REFERENCE/OPOCKET NUMBER: MAC-100C1

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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US-09-582-200A-11
; Sequence 11, Application US/09582200A
; Patent No. 6482609
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Matches 317; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                           Gaps
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                                                                                                                                DB 2; Length 352;
                                                                                                                                                                        Indels
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APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
TITLE OF INVENTION: G-Protein Coupled Receptors
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Belease #1.0, Version #1.25
CURRENI APPLICATION DATA:
APPLICATION NUMBER: US/09/225,024
FILING DATE: 04-JAN-1999
CLLASSIFICATION: 435
PRICA APPLICATION DATA:
APPLICATION NUMBER: 08/760,936
FILING DATE: 6-DEC-1996
PRICA APPLICATION NUMBER: 08/760,936
FILING DATE: 15-FEB-1994
ATORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
                                                                                                                                                    ; Pred. No. 4.6e-131; 13; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                90.0%; Score 1625.5;
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REFERENCE/DOCKET NUMBER: 38,261
RELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
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US-09-225-024-2
; Sequence 2, Application US/09225024
; Patent No. 6518414
                                                                                                                                Query Match
Best Local Similarity 89.8%;
Matches 317; Conservative 1
; SEQ ID NO 24
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Rattus SP.
US-09-169-205D-24
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                                                                                             APPLICANT: NOUSIERS, FECTIONS, AGNUAL, APPLICANT: Vyas, Tejal B.
APPLICANT: Vyas, Tejal B.
APPLICANT: Gupta, Ashwani
FILEREFERENCE: 108074-00002
CURRENT APPLICATION IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
FILER REFERENCE: 108074-000002
CURRENT APPLICATION NUMBER: 09/22,995
PRIOR PILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-11-25
PRIOR FILING DATE: 1998-11-25
PRIOR FILING DATE: 1998-11-25
PRIOR FILING DATE: 1998-11-25
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 14
SSOTHARE: PALENTIN VERSION 3.1
SSOTHARE: PALENTIN VERSION 3.1
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Patent No. 6485922
GENERAL INFORMATION:
APPLICANT: Erikson, James
APPLICANT: Kiefer, Michael
APPLICANT: Kiefer, Michael
TITLE OF INVENTION: ACTIVITY OF AN LPA RECEPTOR
FILE REFERENCE: 252/004
FILE REFERENCE: 1998-10-09
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: rat EDG-4 polypeptide
US-09-582-200A-11
                   APPLICANT: Munroe, Donald G.
APPLICANT: Kamboj, Rajender
APPLICANT: Peters, Diana
APPLICANT: Kooshesh, Fatemeh
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US-09-169-205D-24
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                                                       3 SLYSEYLNPNKVQEHYNYT-KETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARN
                                                                                       62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVF
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  Gaps
12;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,989B
FILING DATE: 15-FEB-1994
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/ACENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REPERENCE/DOCKET NUMBER: MAC-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
  59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 TNKEMRRAFIRIMSC 328
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LENGTH: 383 amino acida
TYPE: amino acid
  Conservative
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APPLICANT: Shelagh Wilson
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APPLICANT: Dillipe Robert
APPLICANT: Nassirah Khandoudi
APPLICANT
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Pred. No. 1.2e-64;
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                                                                                                                                                                                                                                                     90.0%; Score 1625.5; DB 2; 89.8%; Pred. No. 4.6e-131; ive 13; Mismatches 22;
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CURRENT FILING DATE: 1999-03-04
EARLIER APPLICATION NUMBER: 60/077,369
EARLIER FILING DATE: 1998-03-09
EARLIER PILING DATE: 1998-03-09
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 2
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                                                             352 amino acids
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Matches 317; Conservative
  INFORMATION FOR SEQ ID NO:
                                SEQUENCE CHARACTERISTICS
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                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide US-09-225-024-2
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Search completed: December 4, 2005, 06:24:23 Job time : 35.5 secs

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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                                                                                       This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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FUNCTION: Receptor for the lysosphingolipid sphingosine 1-bhosphate (SIP). SIP is a bloative lysophospholipid that elicits diverse physical opical effect on most types of cells and tissues. When expressed in rat HTC4 hepatoma cells, is capable of mediating SIP-induced cell proliferation and suppression of apoptosis. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
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                                                                                                                                                                                                                       R GO; GO:0004330; F:G-protein coupled receptor activity; TAS.

R GO; GO:000289; F:lipid binding; TAS.

R GO; GO:000289; F:lipid binding; TAS.

R GO; GO:000186; P:G-protein coupled receptor protein signalin. .; T.

R GO; GO:000284; P:positive regulation of cell proliferation; TAS.

R GO; GO:0008284; P:positive regulation of cell proliferation; TAS.

R GO; GO:0008284; P:positive regulation of cell proliferation; TAS.

R HOROWOOTS ENDORMED TO TAS.

R PERNY PRONONOTS GPCR. Hoodpsn.

R PRINTS; PRO0137; GPCR. HOODPSN.

R PRINTS; PRO0137; GPCR. HOODPSN.

R PRINTS; PRO0137; GPCR. HOODPSN.

R PROSITE; PSS00237; GPROTEIN RECEP FI 1; 1.

R PROSITE; PSS00237; GPROTEIN RECEP FI 2; 1.

R G-protein coupled receptor; Glycoprotein;

M Multigene family; Palmitate; Receptor; Transmembrane.

T TRANSEM 35 59 1 (Potential).
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S-palmitoyl cysteine (By similarit
N-linked (GlcNac. . ) (Potential)
F -> S (in Ref. 1).
G -> V (in Ref. 1).
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Pred. No. 1.8e-115;
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2 (Potential).
Extracellular (Potential).
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Extracellular (Potential).
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MENL; AF262681; -AAP220652.1; -; Genomic_I

EMBL; BC0695981; AAR69598 1; -; mCN

Ensembl; ENSG00000175898; Homo sapiens.
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Matches 352; Conservative
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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., A Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., A Alaawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Nurshaw-Boris A., Yoshida K., Wang K.H., Weitz C., Whittaker C., Wilming L., Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                     TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
13-SEP-2005 (TrEMBLrel. 21, Last amnotation update)
Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
11brary, clone:0430039A03 product:endothellal differentiation,
sphingolipid G-protein-coupled receptor, 5, full insert sequence
(Endothellal differentiation, sphingolipid G-protein-coupled receptor,
TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
                                                                                                                                                            VFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musnae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                            353
                                                                                                                                                                                                                                                                                                                                                              301 RPLQCWRPGVGVQGRRRGGTPGHHLLPLRSSSSLERGWHMPTSPTFLEGNTVV 353
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                                                                                                                                                                                                                                                                                                                            RPLOCWRPGVGVQGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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The FANTOM Consortium,
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NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Lung;
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Nature 420:563-573(2002).
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Q8C3Q7;
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AECHAGORIAN SEQUENCE.

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      Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Shibata K., Itoh M., "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA ibraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
EMBL; AK065114; BAC39368.1; -; mRNA.
EMBL; BC056760; AAH96760.1; -; mRNA.
                                                                                                                                                                                                                                      STRAIN=C57BL/63; TISSUE=Lung; MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Pujiwake S., Inoue K., Sakaguchi S., Ikegami T., Kashiiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; sequencing pipeline with 384 multicapillary sequencer.";
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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MGI; MGI:99569; Edg5.
GO; GO:0007610; P:behavior; IMP.
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InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR004061; SIP_receptor.
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                                                                                                                                                                                                                                                                                                            61 NSKFHSAMYLFLGNIAASDILLAGVAFVANTILLSGHVTLSLTPVQWFAREGSAFITLSASV 120
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01-FEB-1996 (Rel. 33, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5) (G-protein coupled receptor H218) (AGR16) (Endothelial differentiation G-protein coupled receptor 5) (Sphingosine 1-phosphate receptor 5) (Sphingosine 1-phosphate receptor 2) (S1P2).
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MEDLINE=94373324; PubMed=8087418; DOI=10.1006/mcne.1994.1024;
Maclennan A.J., Browe C.S., Gaskin A.A., Lado D.C., Shaw G.;
"Cloning and characterization of a putative G-protein coupled receptor potentially involved in development.";
Mol. Cell. Neurosci. 5:201-209(1994).
                                                                                                                                                                                                                            1 MGGLYSEYINPEKVLEHYNYTKETLDMQETTSRKVASAFIIILCCAIVVENLLVLIAVAR
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus
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Okazaki H., Ishizaka N., Sakurai T., Kurokawa K., Goto K., Kumada M.,
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           PRINTS; PRO1525; EDGSRECEPTOR.
PRINTS; PR00237; GPCRRHONDEN.
PRONTS; PR01523; SIPRECEPTOR.
PROSITE; PS50262; G_PRO1521N. RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SEQUENCE 352 AA; 38829 MW; 6A3E426B0FE54406 CRC64;
                                                                                                                                                                      ä
                                                                                                                                    2; Length 352;
                                                                                                                                                                      21; Indels
                                                                                                                                     90.3%; Score 1631.5; DB 2 90.4%; Pred. No. 1.1e-103;
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                                                                                                                                                      90.4%; Pred. No. 1.1e ive 12; Mismatches
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                                                                                                                                                        Jest Local Similarity yu. 4
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Pfam; PF00001; 7tm 1; 1.
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                          PHARMACOLOGICAL CHARACTERIZATION.

Pharmacological properties and signal transduction of ancellin N., Hla T.;

Ancellin N., Hla T.;

Ancellin N., Hla T.;

Ancellin N., Hla T.;

Tubiferential pharmacological properties and signal transduction of the sphingosine 1-phosphate receptors EDG-1, EDG-3, and EDG-5.";

J. Biol. Chem. 274:18997-19002(1999).

J. Biol. Chem. 274:
                          An S., Bleu T., Huang W., Hallmark O.G., Coughlin S.R., Goetzl E.J.; "Identification of cDNAs encoding two G protein-coupled receptors for Iysosphingolipids."; FEBS Lett. 417:279-282(1997).
MEDLINE=98072391; PubMed=9409733; DOI=10.1016/S0014-5793(97)01301-X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO1525; EDGSRECEPTOR.
PRINTS; PRO1527; GPCRRHODDEN.
PROSTITE; PRO1523; SIPRECEPTOR.
PROSTITE; PS00237; GPCTEIN RECEP F1 1; FALSE NEG.
PROSTITE; PS50262; G-PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
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S-palmitoyl cysteine (By similarity).
N-linked (GlcNAc. . .) (Potential).
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RGD; 68334; Edg5.
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Interpro; IPR000276; GPCR Rhodpsn.
Interpro; IPR004061; SIP_receptor.
Pfam; PF00001; 7tm 1; 1.
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MEDLINE-93176155; PubMed-8382486;
Okazaki H., Ishizaka N., Sakurai T., Kurokawa K., Goto K., Kumada M.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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Submitted (Ang-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
EMBL; AB016931; BAA32454.1; -; mRNA.
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Best Local Similarity 89.8 Matches 317; Conservative

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Query Match

9 9 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQMPAREGSAFITLSASV 120

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1 MGGLYSEYLNPEKVQEHYNYTKETLDMQETPSRKVASAFIIILCCAIVVENLLVLIAVAR 1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGPVTLSLTPLQWFAREGSAFITLSASV 120
                                                                 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS 180
                                                                                                                                                                                                                                                                                                                                     VPIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
                                                                                                                                                                                                                                                                                                                                                                       241 VFIICWLPAFSILLLDSTCPVRACPVLYKAHYFFARATLNSLLNPVIYTWRSRDLRREVL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P25592; QBR236;
10.0CT-1996 (Rel. 34, Created)
10.0CT-1996 (Rel. 43, Last sequence update)
10.MAY-2005 (Rel. 47, Last annotation G-protein (Lysophospholipid receptor B2) (Endothelial differentiation G-protein coupled receptor 5) (Sphingosine 1-phosphate receptor 2) (SIP2).

Name=Edg5; Synonyms=Gpcr13, Lpb2;
Name=Edg5; Synonyms=Gpc
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                                                                                                                                                                                                                                       181 TVLPLYAKHYVLCVVTIFSVILLAIVALYVRIYFVVRSSHADVAGPQTLALLKTVTIVLG
                                                                                                    181 TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
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-!-SUBCELULAR LOCATION: Integral membrane protein.
-!-TISSUE SPECIFICITY: Most abundant in heart and lung; low, but clearly observed in kidney, liver and thymus; much lower but detectable in brain, testis, stomach and intestine. Not significantly detected in any of the sections of embryonic day (E118, except in embryonic brain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 RPLLCWRQGKGATG-RRGGNPGHRLLPLRSSSSLERGLHMPTSPTFLEGNTVV 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY STRAIN=129/SvJ;
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EMBL; L20334; AAA16846.1; -; mRNA.
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
Receptor; Transducer; Transmembrane.
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Cytoplasmic (Potential).
S-palmitoyl cysteine (By similarity)
N-linked (GlCNAc. . .) (Potential).
P -> S (in Ref. 2).
Q -> K (in Ref. 2).
H -> R (in Ref. 2).
H -> R (in Ref. 2).
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29-MAR-2004 (Rel. 43, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Sphingosine 1-phosphate receptor Edg-5 (SIP receptor Edg-5)
(Sphingosine 1-phosphate receptor 2) (SIP2).
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                  InterPro; IPR004063; EDGS_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IRR004061; SIP_receptor.
Pfam, PF000001; 7tm 1; 1.
PRINTS; PR01525; EDGSRECEPTOR.
PRINTS; PR00237; GPCRRHODOPSN.
GO:0007610; P:behavior; IMP
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90.1%;
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Matches 318; Conservative
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restrictions on
               Eukaryota; Metazoa; Chordata; Cramiata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the Buropean Bioinformatics Institute. There are no restrictions o
use as long as its content is in no way modified and this statement
                                                                   NUCLEOTIDE SEQUENCE, AND VARIANTS MIL HIS-150 AND CYS-167.
MEDLINE=20365730; PubMed=10910360; DOI=10.1038/35018092;
Kupperman B., An S., Osborne N., Waldron S., Stainier D.Y.R.;
"A sphingosine-1-phosphate receptor regulates cell migration during vertebrate heart development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZFIN, ZDB-GENE. 2013-2; edgs.
InterPro; IPR000297; EDG1receptor.
InterPro; IPR000276; GPCR_Rhodgsn.
InterPro; IPR000661; S1P_receptor.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00542; EDG1RECEPTOR.
PRINTS; PR00542; GPCRRHODOPSN.
PRINTS; PR01523; S1PRECEPTOR.
PROSITE; PS00237; GPRRECEPTOR.
PROSITE; PS00237; GPROTEIN_RECEP_F1 1; 1.
Disease mutation; G-protein_coupled_receptor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extracellular (Potential).
1 (Potential).
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4 (Potential).
Extracellular (Potential).
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2 (Potential).
Extracellular (Potential)
3 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lipoprotein; Palmitate; Receptor; Transducer;
          Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF260256; AAF88001.1; -; mRNA.
Ensembl; ENSDARG0000009719; Danio rerio.
                                                                                                                      Nature 406:192-195(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 VIIVLGVFIICWLPAFTILLLDTSCKMKQCPILNNAGIFFSFATLNSALNPLIYTLRSKD 314
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:001619; F:lysosphingolipid and lysophosphatidic acid . . .; IEA.

GO; GO:0001619; F:receptor activity; IEA.

GO; GO:000186; P:receptor activity; IEA.

GO; GO:0007186; P:receptor activity; IEA.

InterPro; IPR000463; EDGS receptor.

InterPro; IPR004063; EDGS receptor.

InterPro; IPR004061; SIP_receptor.

InterPro; IPR004061; SIP_receptor.

InterPro; IPR004061; AIP_receptor.

PFam; PF00001; 7tm_1; 1.
5 (Potential).
Cytoplasmic (Potential).
6 (Potential).
Extracellular (Potential).
7 (Potential).
Cytoplasmic (Potential).
S-pamitoyl cysteine (By similarity).
N-linked (GlcNAc. . .) (Potential).
R -> H (in mil; allele m93; lack of S1P-mediated signaling).
R -> C (in mil; allele te273; lack of S1P-mediated signaling).
N- C (in mil; allele te273; lack of S1P-mediated signaling).
                                                                                                                                                                                                                                                                                  SLYSEYLNPNKVQEHYNYTKE-----TLETQETTSRQVASAFIVILCCAIVVENLLV
                                                                                                                                                                                                                                                                                                                           LIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFI
                                                                                                                                                                                                                                                                                                                                                                                                                                           175 HLEACSTVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKT
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
Endothelial differentiation sphingolipid G-protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cavia porcellus (Guinea pig).
Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                     73; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
STRAIN-hartley; TISSUE-Myenteric plexus;
Segura B.J., Xiao L., Cowles R.A., Turner D.J., Logsdon C.D.,
Mulholland M.M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                           DB 1; Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315 MRKEFLRVLCCW-----GLLNCGRPPHRCMVPLKSSSSME 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 LRREVLRPLQCWRPGVGVQGRRRGGTPGHH-LLPLRSSSSLE 335
                                                                                                                                                                                                                       ; Pred. No. 2.4e-60; 51; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 AA.
                                                                                                                                                                                                           Score 998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                             370 AA; 41777 MW;
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Q91XRO;
                                                                                                                                                                                                                       Best Local Similarity 58.5
Matches 200; Conservative
    235
254
275
275
289
310
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325
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    215
236
236
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An outside A. Albert R., Mongmayer P., Schupp I., Wellenreuther R.,

RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

Ra Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.

C. -- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

T. -- SIMILARITY: Belongs to the G-protein coupled receptor I family.

EMBL; CR860217; CAH92159.1; -; mRNA.

RG; GO:00016021; C:integral to membrane; IEA.

RG; GO:0001619; F:iysosphingolipid and lysophosphatidic acid . .; IEA.

RG; GO:0001619; F:iysosphingolipid and lysophosphatidic acid . .; IEA.

RG; GO:0001619; F:iysosphingolipid and lysophosphatidic acid . .; IEA.

RG; GO:0001619; F:iysosphingolipid and lysophosphatidic acid . .; IEA.

RG; GO:0001619; F:iysosphingolipid and lysophosphatidic acid . .; IEA.

RG; GO:0001619; F:iysosphingolipid and lysophosphatidic acid . .; IEA.

RG; GO:0001619; F:iysosphingolipid and lysophosphatidic acid . .; IEA.

RG; GO:0001619; F:isggnal transduction; IEA.

InterPro; IPR00276; GPCR_Rhodpsn.

InterPro; IPR004061; SIP_Receptor.

InterPro; IPRN04061; SIP_Receptor.

R PANTHER; PFHRH19266; EBGIreceptor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVOWFAREGSAFITLSASVF 121
                                                                                                                                                                                                                                                           94 GSVTLRLTPVQWFAREGSAFITLSASVFSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIG 153
                                                                                                                                                                     14 $SVSDYVNYDIIVRHYNYTGKLNISADKENSIKLTSVVFILICCFIILENIFVLLTIWKT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pongo pygnaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 SLYSEYLNPNKVQEHYNYT-KETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARN
                                              154 ASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSIILLAIVALYVRIY
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PRINTS; PR00642; EDGIRECEPTOR.

PRINTS; PR01148; EDGIRECEPTOR.

PRINTS; PR0123; GPCRRHODOPSN.

PRINTS; PR01523; SIPRECEPTOR.

PROSTITE; PS00237; GPROTEIN RECEP_F1_1; 1.

G-protein coupled receptor; Hypothetical protein; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.4%; Score 856; DB 2; Length 382;
51.4%; Pred. No. 1.3e-50;
ive 58; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42773 MW; 6F0841D0E93789CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein DKFZp469M1119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fransmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSR7A1 PONPY PRELIMINARY;
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Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               274 FAVSTLNSLL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAFATLNSLL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=DKFZp469M1119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LLAGVARIANTLLSGSVTLQLTPVEWFAREGSAF1TLSASVFSLLAIAIERHVAIAKVVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YGSDKSCRMLLLIGASWVILLVIGGLPILGWNCIGRLDTCSTVLPLYAKQYVLCVVTIFS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 LLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVFSLLAIAIERHVAIAKVKL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 YGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YTKETLDVRETTSRQVASAFIVILCCAIVVENLLVLVAVGRNSKLHSAMYLFLGNLAASD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 YTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARNSKFHSAMYLFLGNLAASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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PRINTS; PR01525; EDGSRECEPTOR.
PRINTS; PR01523; GPCRHODOPSN.
PRINTS; PR01523; SIPRECEPTOR.
PROSTIE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
PRINTS; PRO1525; EDGERECEPTOR.
PRINTS; PRO0237; GPCRRHODOPSN.
PRINTS; PRO1523; SIPRECEPTOR.
PROSITE; PS50262; G_PROTEIN RECEP F1 1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
NOW TER 202 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Sprague-Dawley/Had;
Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;
EMBL; AR090995; AAG24259.1; -: mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001186; P:lysosphingolipid and lysophosphatidic acid ...
GO; GO:0007186; P:greepton activity; IEA.
GO; GO:0007186; P:signal transduction; IEA.
InterPro; IPR004063; EDG5_receptor.
InterPro; IPR004061; SIP_receptor.
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                                                                                                                                                                                                                                                                                                                                          Length 202;
                                                                                                                                                                                                                                                                                                                                   Query Match 51.7%; Score 933; DB 2; Length 20
Best Local Similarity 91.6%; Pred. No. 3.8e-56;
Matches 185; Conservative 9; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                        21836 MW; D9814EC85B42320A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 16, Last sequence update)
Putative G-protein coupled receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 IILLAIVALYVRIYCVVRSSHA 221
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                                                                                                                                                                                                                                                                        202 AA;
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Matches 169;
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ID EDG1
AC 04-83
DT 01-87
DT 01-8
DT 10-M
DE Sphi
DE Sphi
DE Ratt
OC MAMMO
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altauner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altachul S.F., Zeeberg B., Buerlow K.H., Schaefer C.F., Bhat N.K.,
Aptschul S.F., Zeeberg B., Buerlow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Abatchench L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarene P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachigues S., Worley K.C., Sheer E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Browns R. Roder M. A., Schein J.E., Jones S.J.M., Marra M.A.,
Schein J.S., Jones S.J.M., Marra M.A.,
Schein J.S., Jones S.J.M., Marra M.A.,
                                                                                                                                                                             194 VLPLYHKHYILFCTTVFTLLLLSIVILYCRIYSLVRTRSRRLTFRKNISKASRSSEKSLA 253
                                                                                                                                                                                                                                                                254 LLKTVIIVLSVPIACWAPLFILLLLDVGCKVKTCDILFRAEYFLVLAVLNSGTNPIIYTL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                 SHADMAAPQTLA
                      SLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACST
                                                                                                                                                                                                                                  LLKTVTIVLGVFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
G protein-coupled sphingolipid receptor (EDG1 protein) (Endothelial differentiation, sphingolipid G-protein-coupled receptor, 1)
Name=CHEDG1; Synonyms=EDG1; ORFNames=RP4-575N6.1-001;
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tigyi G.J. Sr., Wang D. Sr.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 AA.
                                                                                                                                                                                                                                                                                                                                                                           314 TNKEMRRAFIRIMSC 328
                                                                                                                                                                                                                                                                                                                                          291 RSRDLRREVLRPLQC 305
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Q9NYN8; Q9BYY4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .; IEA.
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

EMBL; AR513165; AR443420.1; -; mRNA.

EMBL; CR541786; CAG46585.1; -; mRNA.

EMBL; CR541786; CAG47065.1; -; mRNA.

EMBL; AL109741; CAG121801.1; -; Genomic_DNA.

EMBL; AL109741; CAG1801.1; CAG1801
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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10-MAY-2005 (Rel. 47, Last annotation update)
Sphingosine 1-phosphate receptor Edg-1 (Sphingosine 1-phosphate receptor 1) (SIP1)
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SLYSEYLNPNKVQEHYNYT-KETLETQETTSRQVASARIVILCCAIVVENLLVLIAVARN 61

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                                                            MEDLINE=95047498; PubMed=7959012; DOI=10.1016/0378-1119(94)90171-6; A. Lado D.C., Browe C.S., Gaskin A.A., Borden J.M., Maclennan A.J.; Lado D.C., Browe C.S., Gaskin A.A., Borden J.M., Maclennan A.J.; "Cloning of the rat edg-1 immediate-early gene: expression pattern "cloning of the rat edg-1 immediate-early gene: expression pattern graphs of the rat edg-1 immediate early gene: expression pattern angiores diverse functions."; Gene 149:331-336(1994).

I. Gene 149:331-336(1994).

I. FUNCTION: Receptor for the lysosphingolipid sphingosine 1-phosphate (SIP). SIP is a bloactive lysophospholipid that elicits diverse physiological effect on most types of cells and tissues. This inducible epithalial cell G-protein-coupled receptor may be involved in the processes that regulate the differentiation of heteromeric G proteins (BP similarity).

I. SUBCELUULAR LOCATION: Integral membrane protein.

I. DEVELOPMENTAL STAGE: First detected at embryonic day 15. At postnatal day 14 detected in skin, spleen, liver, kidney, heart, testicle, lung and brain. At adulthood is most abundant in brain.

I. SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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S-palmitcyl cysteine (By similarity).
N-linked (GlcNAc. . .) (Potential).
1090BA6AEE09DB4F3 CRC64;
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PRINTS; PR01148; EDGZRECEPTOR.
PRINTS; PR01237; GPCRRHODOPEN.
PRINTS; PR01523; SIPRECEPTOR.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS00262; G_PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.9%; Score 847; DB 1; Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0004930; F:G-protein coupled receptor activity; T:GO:0004946; P:endothelial cell differentiation; IEP. GO:0019182; P:neuron differentiation; IEP. GO:0019226; P:transmission of nerve impulse; IEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (Potential).
Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 (Potential).
Cytoplasmic (Potential).
6 (Potential).
Extracellular (Potential).
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Extracellular (Potential)
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InterPro; IPR002277; EDG2_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR004061; SIP_receptor.
PANTHER; PTHR19266:SF5; EDGIreceptor; 1.
Pfam; PF00001; 7tm 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U10303; AAA83418.1; -; mRNA.
PIR; I53870; I53870.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 AA;
 NCBI_TaxID=10116;
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Gaps

14;

60; Mismatches 103; Indels

Pred. No. 5.3e-50;

48.78;

Conservative

Best Local Similarity Matches 168; Conserv

Query Match

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MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

A Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul R.F., Jordan H., Moore T. Max S.I., Wang J., Hsleh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raple S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimmood J.W., Schmutz J., Mysrs R.M.,

Rodriguez A.C., Grimmood J.W., Schmutz J., Wysrs R.M.,

Rotherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

B. W. Genneration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                         SLLAIAIAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACST
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
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--- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
--- SIMILARITY: BEJONGS to the G-protein coupled receptor 1 family.
EMBL; BCO97938; AAN97938.1; -; mRNA.
InterPro; IPR000987; EDG1receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Endothelial differentiation sphingolipid G-protein-coupled receptor
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                                                                                                                                                                                                                                   74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
clone:1200004816 product:endothelial differentiation sphingolipid G-
protein-coupled receptor 1, full insert sequence (Endothelial
differentiation sphingolipid G-protein-coupled receptor 1).
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|SLAIAIERYITWLKWKLHNGSNSSRSFLLISACWVISLILGGLPIMGWNCISSLSSCST
                                                                                                                                                                                                                                                                                                                                                                        3 SLYSEYLNPNKVQEHYNYT-KETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARN
                                                                                                                                                                                                                                  SQVSDYGNYDIIVRHYNYTGKLNIGVEKDHGIKLTSVVFILICCLIILENIFVLLTIWKT
                                                                                                                                                                                                                                                           SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C5BL/67; TISSUB=Lung;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6J; TISSUE=Lung, MEDLINE=21085500; MEDLINE=21085600; Pubmed=11217851; DOI=10.1038/3505500; MEDLINE=2108560; Pubmed=11217851; DOI=10.1038/3505500; MEDLINE=21.08560; Pubmed=1127851; Schino M., Itch M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
       InterPro; IRRO0276; GPCR_Rhodpen.
InterPro; IRR000276; GPCR_Rhodpen.
Pfam; PF00001; Thm 1; IP_receptor.
PRINTS; PR00142; EDGIRECEPTOR.
PRINTS; PR00148; EDG2RECEPTOR.
PRINTS; PR00123; GPCRHODOPSN.
PROSITE; PS002237; GPROTEIN RECEP_FI_2; I.
PROSITE; PS002237; GPROTEIN_RECEP_FI_2; I.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 383 AA; 42746 MM; 090BA6AEE09DB4F3 CRC64;
                                                                                                                                                                                    14;
                                                                                                                                                             Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 TNKEMRRAFIRIISCCKCPNGDSAGKFKRPIIPGMEFSRSKSDNS 359
                                                                                                                                                         46.9%; Score 847; DB 2; Length 38:
48.7%; Pred. No. 5.3e-50;
tive 60; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 RSRDLRREVLRPLOCWR-PGVGVQGR-RRGGTPGHHLLPLRSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                  Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muridae, Murinae, Mus.
                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Edg1;
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Redoc R., Okazaki Y., Goloboli T., Bondon H., Kankuan T., Salto R.,

Redoc R., Wattsudd H.A., Ashburner H., Batalow S., Comavant T.,

Redoc R., Wattsudd H.A., Ashburner H., Batalow S., Comavant T.,

Redoc R., Wattsud H.A., Ashburner H., Batalow S., Comavant T.,

Redol D., Gudo T., Batalo F., Sixuki R., Tomita M., Wagner L., Washio T.,

Sharimal L.M., Stabili F., Suxuki R., Tomita M., Wagner L., Washio T.,

Sharimal L.M., Stabili F., Suxuki R., Tomita M., Wagner L., Washio T.,

Sharimal L.M., Stabili P., Suxuki R., Tomita M., Wagner L., Washio T.,

Batalo C., Gudo T., Puruno M., Modriguez I., Sakamoto N.,

Batalo C., Ring B., Ringwald M., Nodriguez I., Sakamoto N.,

Batalo C., Ring B., Ringwald M., Nodriguez I., Sakamoto N.,

Bataki H., Sato C., Scheenbach C., Saya T., Shirkar Y., Scotch K.-F.,

Bataki H., Sato C., Scheenbach C., Saya T., Shirkar Y., Scotch K.-F.,

Bataki H., Sato C., Scheenbach C., Saya T., Shirkar Y., Scotch K.-F.,

Bataki H., Sato C., Scheenbach C., Saya T., Shirkar Y., Scotch K.-F.,

Bataki H., Sato C., Scheenbach C., Saya T., Shirkar Y., Scotch K.-F.,

Bataki H., Sato C., Scheenbach C., Saya T., Shirkar Y., Scotch K.-F.,

Bataki H., Sato C., Scheenbach C., Saya T., Shirkar Y., Scotch K.-F.,

Bataki H., Sato C., Scheenbach C., Saya T., Shirkar Y., Scotch K.-F.,

Bataki H., Sato M., Satolaka T., Matauda H., School H., Rodol S.,

Remandar A., Satolin M., Satolaka T., Mana M., School H., Shirkar M., Satolaka T., Satolin H., Satolaka T., Satolin H., Satolaka T., Satolin H., Satolaka T., Satolin H., Satolaka T., ```

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  STRAIN-C57BL/6; TISSUB-Eye, and Mouse;

XX STRAIN-C57BL/6; TISSUB-Eye, and Mouse;

XR STRAIN-C57BL/6; PubMed=12477932; DOI=10.1073/pnas.242603899;

XR STRAIN-C57BL/6; PubMed=12477932; DOI=10.1073/pnas.242603899;

XR STRAIN-C57BL/6; Feingold E.A., Grouse L.H., Derge J.G.,

XR Altschul S.F., Zeeberg B., Bactow K.H., Schaefer C.F., Bhat N.K.,

XR Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Dopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Robards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XR Stoken S.A., McEwan D., Sodergren B.J., Lu X., Gibbs R.A.,

R Halton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Halton D.K., Muzny D.M., Scherchenko Y., Bouffard G.G.,

A Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R Schnerth A., Schein J.E., Jones S.J.M., Marra M.A.;

R Generaticed Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

A Monton and initial analysis of more than 15,000 full-length human
   EMBL; AK004591; BAB23393.1; -; mRNA.
EMBL; BC049094; AAH49094.1; -; mRNA.
EMBL; BC045093; AAH50094.1; -; mRNA.
EMBL; BC045003; AAH51023.1; -; mRNA.
EMBL; BC045003; AAH51023.1; -; mRNA.
MGI; MGI:1096355; Edgl.
MGI; MGI:1096355; Edgl.
MGI; MGI:0016021; C:integral to membrane; TAS.
GO; GO:0010525; P:anglogenesis; IDA.
GO; GO:0001535; P:regulation of cell adhesion; IDA.
                           Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukunishi Y., Furuno M., Hanagaki T., Hara A. Hayatu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yammura T., Yasunishi A., Yoshida K., Yoshino M., Muramateu M., Hayashizaki Y.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
   InterPro; IPRO0227; EDG2 receptor.
InterPro; IPRO0227; EDG2 receptor.
InterPro; IPRO0227; EDG2 receptor.
InterPro; IPRO0227; EDG2 receptor.
InterPro; IPRO04061; SIP receptor.
InterPro; IPRO04061; SIP receptor.
R PANTHER; PTHA1926; SF5; EDG1receptor; 1.
R PANTHER; PRO1642; EDG1RECEPTOR.
R PRINTS; PRO1643; EDG2RECEPTOR.
R PRINTS; PRO1623; SIPRECEPTOR.
R PRINTS; PRO1623; GPRCHEIN RECEP F1 1; UNKNOWN 1.
R PROSITE; PS0237; GPRCTEIN RECEP F1 2; 1.
R PROSITE; PS05042; GPRCTEIN RECEP F1 2; 1.
R PROSITE; PS05042; A18650404; Receptor; Receptor; Transmembrane.
SEQUENCE 332 AA; 42639 MW; SFEAC9A2BD65CB2A CRC64;
   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
  Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
  TISSUE=Eye;
Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
   STRAIN=C57BL/6; TISSUE=Mouse;
  ведиепсев."
  NUCLEOTIDE SEQUENCE.
   NUCLEOTIDE SEQUENCE
                NUCLEOTIDE SEQUENCE
   NUCLEOTIDE SEQUENCE
  mouse cDNA
   Strausberg R
  and
   8
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SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVF 121
  SLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACST 181
   VLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRS------SHADMAAPQTLA 230
  231 LLKTVTIVLGVFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTW 290
   JUNEARITY: Belongs to the G-protein coupled receptor 1 family.

-1. SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

-1. SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

-1. SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

EMBL; BT021184; AAX3136-1; -; mRNA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0001619; F:lysosphingolipid and lysophosphatidic acid . . .; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
  73
   14 SSVSDYGNYDIIVRHYNYTGKLNIGAEKDHGIKLTSVVFILLICCFIILENIFVLLTIWKT
   3 SLYSEYLNPNKVQEHYNYT-KETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARN
  10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
Endothelial differentiation, sphingolipid G-protein-coupled receptor,
  MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101; Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T., Casas B., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L., Hearon M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G., Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
   Gaps
   T.P.L.;
  Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
  "Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle.";
   14;
   Harhay G.P., Sonstegard T.S., Van Tassell C.P., Clawson M.L., Heaton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T. "Sequencing and analysis of Bos taurus full-length insert CDNA
      Length 382;
; Score 845; DB 2; Length 382;
; Pred. No. 7.3e-50;
60; Mismatches 103; Indels
  291 RSRDLRREVLRPLQCWR-PGVGVQGR-RRGGTPGHHLLPLRSSSS 333
  314 TNKEMRRAFIRIVSCCKCPNGDSAGKFKRPIIPGMEFSRSKSDNS 358
  Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
  382 AA
  PRT;
   Pecora; Bovidae; Bovinae; Bos.
   Genome Res. 11:626-630(2001).
46.8%;
      Query Match
Best Local Similarity 48.7%
Matches 168; Conservative
   QSBIPO BOVIN PRELIMINARY;
QSBIPO;
   NUCLEOTIDE SEQUENCE.
  NUCLEOTIDE SEQUENCE.
   NCBI_TaxID=9913;
   TISSUE=Pooled;
  TISSUE=Pooled
  Keele J.W.;
  62
  254
  122
  182
  clones."
   BOVIN
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   VLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRS-----SHADMAAPQTLA 230
  SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVF 121
   74 KKFHRPMYYFIGNLALSDLLAGVAYIANLLLSGATTYKLTPAQWFLREGSMFVALSASVF 133
   181
   61
  73
   3 SLYSEYLNPNKVQEHYNYT-KETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARN
   SLLAIAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACST
  LLKTVTIVLGVFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTW
   Maucell E. Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Briemont C., Skalli Z., Cattollco L., Poulain J., De Berardinis V., Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff JN., Guigo R., Nusbaum C., Kabinson-Rechavi M., Lindblad-Toh K., Birren B., Nusbaum C., Kabn D., Robinson-Rechavi M., Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
  Gaps
          R InterPro; IPR002277; EDG1receptor.
R InterPro; IPR002277; EDG2 receptor.
R InterPro; IPR004275; EDG1RECEPTOR.
R PANTHER; PR00424; EDG2RECEPTOR.
R PRINTS; PR0148; EDG2RECEPTOR.
R PRINTS; PR01523; SIPRECEPTOR.
R PRINTS; PR01523; SIPRECEPTOR.
R PRINTS; PR01523; SIPRECEPTOR.
R PROSITE; PS02237; GPROTEIN RECEP FI 1; 1.
R PROSITE; PS050262; G PROTEIN RECEP FI 2; 1.
R G-protein coupled receptor; Receptor; Transmembrane.
C SEQUENCE 382 AA; 42742 MW; 31FCB6164ABB12C6 CRC64;
  13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF7591, whole genome shotgun sequence.
ORFNames-GSTENG00004794001;
Tetraodon nigroviridis (Green puffer).
Bukaryota; Metazoa; Chromata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Roteleostomi;
Actinopterygii; Neopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
NCBI_TaxID=99883;
  12;
   Length 382;
   86; Indels
   46.7%; Score 844; DB 2; 50.8%; Pred. No. 8.5e-50;
   50.8%; Preu. ...
   314 SNKEMŘRAFVŘIMSČ 328
   291 RSRDLRREVLRPLQC 305
  2 TETNG
Q4T9E2_TETNG PRELIMINARY;
  160; Conservative
   Similarity
   NUCLEOTIDE SEQUENCE
  62
   122
  182
   254
   Query Match
  Best Local
Matches 16
   RESULT 15
0479E2 TET
10 13-SE
DT 13-SE

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236
  296
  309
   70 NIALSDILAGVVYTANIILISGANTYKLTPTQWFFREGSMFVALAASVFSLLAIAIERHLT 129
   249
  297 REVLRPLQC------WRPGVGVQ-GRRRGGTPGHHLLPLRSSSSLERGMHMPTS- 343
  74 NLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVFSLLAIAIERHVA 133
   134 IAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLC 193
  310 RAFLKTLLCCTACLRPKATFTSPIMGAEFSRSRSDNSSH---PTR----EDGEHSPRGR 361
   69
  73
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype."; Nature 431:946-957(2004).
   10 ISKHYNYTGKFRKIQEDSGLKADSVVPIIVCCFIILENILULTTIWRIKKFHKDMYYFIG
   250 IVLSCPIACWAPLFVLLLLDTACQTLSCPILYKAEWFLALAVINSAMNPLIYTLTSNEWR
   194 VVTIFSIILLAIVALYVRIYCVVR-----SSHADMAAPQTLALLKTVT
  237 IVLGVFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLR
  14 VQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARNSKFHSAMYLFLG
  Gaps
  preliminary data.
--- SUBCELLULAR LOCATION: Integral membrane protein (By similarity)
--- SUBICELLULAR LOCATION: Integral membrane protein (By similarity)
--- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
EMBL: CAABO1007591; CAF90490.1; -; Genomic_DNA.
InterPro; IPR000987; EDGIreceptor.
InterPro; IPR0004061; SIP_receptor.
InterPro; IPR004061; SIP_receptor.
  PERUNTS; PR0001; 7tm 1; 1.

PRINTS; PR00642; EDGIRECEPTOR.

PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR01523; S1PRECEPTOR.

PROSITE; PS02023; GPROTEIN RECEP F1 1; 1.

PROSITE; PS50262; GPROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 373 AA; 41706 MW; CE779CA9B3D371EB CRC64;
  Genoscope, Whitehead Institute Centre for Genome Research;
Submitted (FBS-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
  38;
  53; Mismatches 104; Indels
  46.6%; Score 841; DB 2; 47.3%; Pred. No. 1.3e-49;
  completed: December 4, 2005, 06:52:03
  Matches 175; Conservative
  353
   362 RTASSGNVTL 371
  344 PTFLEGNTVV
   Best Local Similarity
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model

December 4, 2005, 06:38:17; Search time 24.5 Seconds (without alignments) 1386.307 Million cell updates/sec Run on:

US-10-084-507B-17 1806 1 MGSLYSEYLNPNKVQEHYNY......LERGWHMPTSPTFLEGNTVV 353 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\* Database :

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 24         | Description      | le G   | ģ      | G protein-coupled | sphingosine 1-phos | G protein-coupled | G protein-coupled | lysophosphatidic a | melanocortin 3 rec | G protein-coupled | melanocortin recep | G protein-coupled | probable G protein | melanocortin recep | G protein-coupled | cannabinoid recept | melanocortin recep | melanocortin recep | melanocortin-5 rec | melanocortin 1 rec | melanocortin 5 rec | melanocortin recep | cannabinoid recept | cannabinoid recept | cannabinoid recept | adenosine receptor | MSH receptor - bov | melanocortin 1 rec | ~      | halunorain-uniad |
|------------|------------------|--------|--------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|------------------|
| SOUTHWATES | ID               | JC1465 | 153870 | A35300            | JC7559             | E48909            | JC5245            | JC5293             | \$43850            | 165990            | B46647             | A55689            | 548697             | 836636             | S40454            | A33117             | JC2193             | A57055             | 149008             | S71420             | JC5592             | JN0764             | S70364             | S17595             | 836750             | A48978             | S45708             | 870005             | A48974 | S18444           |
|            | DB               | 7      | ~      | ~                 | ~                  | ~                 | 7                 | ~                  | N                  | 7                 | 7                  | N                 | ~                  | 7                  | ~                 | ď                  | ~                  | 7                  | N                  | ~                  | ~                  | 7                  | ~                  | ~                  | N                  | ~                  | ~                  | ~                  | ~      | c                |
|            | Length           | 352    | 383    | 381               | 362                | 180               | 378               | 364                | 323                | 362               | 360                | 330               | 363                | 323                | 330               | 473                | 325                | 332                | 372                | 314                | 325                | 325                | 347                | 472                | 360                | 412                | 317                | 314                | 410    | 320              |
| de         | . Query<br>Match | 90.0   | 46.9   | 46.3              | 45.3               | 44.8              | 42.6              | 27.9               | 19.5               | 19.3              | 19.3               | 19.2              | 18.9               | 18.7               | 18.7              | 16.7               | 16.6               | 16.5               | 16.4               | 16.4               | 16.4               | 16.2               | 16.2               | 15.9               | 15.8               | 15.8               | 15.8               | 15.7               | 15.7   | 7                |
|            |                  | 1625.5 | ന      | 836.5             | 817.5              | 809               | 769               | 504                | 352.5              | 349               | 348.5              | 347               | 340.5              | 338.5              | 338               | 302                | 300                | 298.5              | 297                | 296.5              | 296.5              | 292.5              | 292.5              | 288                | 286                | 285.5              | œ                  | 283.5              | മ      | 281.5            |
|            | Result<br>No.    | 1      | 7      | ٣                 | 4                  | ß                 | 9                 | 7                  | 80                 | 6                 | 10                 | 11                | 12                 | 13                 | 14                | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 | 24                 | 25                 | 26                 | 27                 | 28     | 29               |

| melanocyte-stimula | melanocyte stimula | A2 adenosine recep | melanocyte-stimula | melanotropin recep | G protein-coupled | alpha-1A-adrenergi | alpha-1A-adrenergi | adrenocorticotropi | adrenocorticotropi | alpha-1-adrenergic | alpha-1A adrenergi | adenosine A2a rece | adrenocorticotropi | 5-HT4S receptor - | serotonin 4 recept |
|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|
| S25581             | T12055             | 148095             | 146416             | S29204             | D30341            | JH0447             | 139369             | 152326             | JC4046             | A40491             | A38731             | S68247             | C43265             | S55550            | S55549             |
| 0                  | N                  | N                  | N                  | N                  | ~                 | ~                  | ~                  | ~                  | ~                  | ~                  | N                  | ~                  | ~                  | ~                 | ~                  |
| 15                 | 317                | 409                | 325                | 317                | 412               | 501                | 572                | 296                | 296                | 515                | 260                | 409                | 297                | 387               | 406                |
| m                  |                    |                    |                    |                    |                   |                    |                    |                    |                    |                    |                    |                    |                    |                   |                    |
|                    | 15.5               | 15.5               | 15.1               | 15.1               | 15.0              | 14.9               | 14.9               | 14.8               | 14.8               | 14.7               | 14.5               | 14.4               | 14.3               | 14.2              | 14.2               |
|                    |                    | 279.5 15.5         |                    |                    | 271.5 15.0        |                    |                    | 268 14.8           |                    |                    | 261 14.5           |                    | 257.5 14.3         |                   |                    |

## ALIGNMENTS

| <br>RESULT 1              |                                                                                                                                                 |
|---------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|
| <br>JC1465                |                                                                                                                                                 |
| probable                  | probable G protein-coupled receptor - rat<br>C. Speries: Pathus normericus (Norman rat)                                                         |
| C, Date:                  | C.Date: 0. Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004                                                                     |
| <br>C, ACCESS<br>R,Okazak | Cinceessin: Octaos<br>Riokazaki, H.; Ishizaka, N.; Sakurai, T.; Kurokawa, K.; Goto, K.; Kumada, M.; Takuwa, Y                                   |
| Biochem.<br>A; Title:     | Biochem. Biophys. Res. Commun. 190, 1104-1109, 1993<br>A;Title: Molecular cloning of a novel putative G protein-coupled receptor expressed in t |
| A;Refere                  | A;Reference number: JC1465; MUID:93176155; PMID:8382486<br>A:Accession: JC1465                                                                  |
| <br>A; Molecu             | A; Molecule type: mRNA                                                                                                                          |
| A, Cross-                 | A,Cross-references: UNIPROT:P47752; UNIPARC:UPI000000001D; GB:AB016931; NID:g3445557; PI                                                        |
| A; Experi                 | A;Experimental source: aortic smooth muscle<br>C.Superfamily. G protein-coupled receptor edg-1                                                  |
| <br>C, Keywor             | C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot                                                        |
| <br>F;67-95/              | Domain: transmembrane #status predicted <tm2></tm2>                                                                                             |
| F,110-12                  | 8/Domain: transmembrane #status predicted <tm3></tm3>                                                                                           |
| F;148-17<br>F;190-21      | F;148-173/Domain: transmembrane #status predicted <1M4><br>F:190-210/Domain: transmembrane #status predicted <tm5></tm5>                        |
| F;234-25                  | #status predicted                                                                                                                               |
| <br>F;272-29              | F;272-293/Domain: transmembrane #status predicted <tm7><br/>5.10/binding site. carbobydrate (len) (royalent) #status predicted</tm7>            |
| F;142,14<br>F;313/Bi      | (2/Binding site: p. hr) (covalent) #s                                                                                                           |
| <br>Query Match           | 90.08;                                                                                                                                          |
| Best Loc<br>Matches       | Best Local Similatity 89.8%; Pred. No. 1.58-12;<br>Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;                               |
| λ                         | 1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR 60                                                                               |
| <br>q                     | 1 MGGLYSEYLNPEKVQEHYNYTKETLDMQETPSRKVASAFIIILCCAIVVENLLVLIAVAR 60                                                                               |
| ò                         | 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120                                                                             |
| <br>qq                    | 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGPVTLSLTPLQWFAREGSAFITLSASV 120                                                                             |
| ò                         | 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS 180                                                                            |
| <br>qa                    | 121 FSLLAIAIERQVAIAKVKLYGSDKSCRMLMLIGASWLISLILGGLPILGWNCLDHLEACS 180                                                                            |
| <br>&.                    | 181 TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAARQTLALLKTVTIVLG 240                                                                            |
| Db                        | LLAIVALYVRIYFVVRSSE                                                                                                                             |
| <br>δλ                    | WEPAFSILLIDYACPV                                                                                                                                |
| qq                        |                                                                                                                                                 |
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sphingosine 1-phosphate receptor - zebra fish
Nyllernate names: endothelial differentiation gene 1 receptor
CjSpecies: Brachydanio rerio (zebra fish)
CjDate: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
CjAccession: JG7559
Rjim, DS.; Ungar, A.R.; Lynch, K.R.
Biochem. Biophys. Res. Commun. 279, 139-143, 2000
A;Title: Characterization of a zebrafish (Danio rerio) sphingosine 1-phosphate receptor A;Reference number: JG7559; MUID: 20563813; PMID:11112429
A;Accession: JG7559
A;Access
   <u>.,</u>
  244
   74 NLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVFSLLAIAIERHVA 133
   124
  193
   240
  241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
  133
   181
   193
  231
   291
  121
  73
  64
  73
   74 KKFHRPMYYFIGNLALSDLLAGVAYTANLLLSGATTYKLTPAQWFLREGSMFVALSASVF
  S IARHYNFTGKFRKVHKDPGLKADSVVFIIVCCFIILENVLVLLTIWRTKKFHKPMYYFIG
  65 NIALSDILAGVVYTANILLSGANTYKLTPTQWFFRGSMFVALAASVFSLLAIAIERHLT
   62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVF
   122 SLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACST
  LKTVTIVLGVFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWR
  134 IAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLC
   194 VVTIFSIILLAIVALYVRIYCVVRSSH------ADMAAPQTLALLKTVTIVLG
  3 SLYSBYLNPNKVQEHYNYT-KETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARN
  14 VQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARNSKFHSAMYLFLG
  182 VLPLYAKHYVLCVVTIFSIILLLAIVALYVRIYCVVRSSHADMA------APQTLAL
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  Gaps
  21;
  Length 362;
  A,Gene: edg1
C,Superfamily: G protein-coupled receptor edg-1
C,Keywords: G protein-coupled receptor; transmembrane protein
   Indels
   Indels
   45.3%; Score 817.5; DB 2;
45.6%; Pred. No. 1.9e-59;
tive 63; Mismatches 109;
                       Pred. No. 5.7e-61;
; Mismatches 87;
50.0%; Pre-
   SRDLRREVLRPLQC 305
  314 NKEMRRAFIRIMSC 327
  Query Match
Best Local Similarity 45.64
Matches 162; Conservative
  Conservative
                   Best Local Similarity
Matches 157; Conserv
  232
   292
  125
   245
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C;Genetics
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   RESULT 3
A35300
G protein-coupled receptor edg-1 - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: A35300
R;Hla, T; Maciag, T.
J. Biol. Chem. 265, 9308-9313, 1990
A;Title: An abundant transcript induced in differentiating human endothelial cells encod
A;Recession: A35300
A;Molecule type: mRNA
A;Recession: A35300
A;Molecule type: mRNA
A;Recidues: L-381 <-HLA>
A;Recidues: L-381 <-HLA>
A;Recidues: L-381 <-HLA>
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C;Genetics:
C;Genetics
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  PII
   Edg-1 orphan receptor - rat
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C,Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I53870
R;Lado, D.C.; Browe, C.S.; Gaskin, A.A.; Borden, J.M.; MacLennan, A.J.
Gene 149, 331-336, 1994
A;Title: Cloning of the rat edg-1 immediate-early gene: expression pattern suggests di
A;Title: Cloning of the rat edg-1 immediate-early gene: expression pattern suggests di
A;Reference number: I53870
A;Reference number: I53870
A;Reference number: I53870
A;Residues: I-383 cRES>
A;Cross-references: UNIRROT:P48303; UNIPARC:UP10000129BD0; EMBL:U10303; NID:g595396; I
C;Superfamily: G protein-coupled receptor edg-1
   121
  134
   181
   SLIAIAIERYITMLKWKLHNGSNSSRSFLLISACWVISLILGGLPIMGWNCISSLSSCST 194
   LLKTVTIVLGVFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTW 290
   61
   SQVSDYGNYDIIVRHYNYTGKLNIGVEKDHGIKLTSVVFILLCCLIILENIFVLLTIWKT 74
  KKFHRPMYYFIGNLALSDLLAGVAYTANLLLSGATTYKLTPAQWFLREGSMFVALSASVF
  SLYSEYLNPNKVQEHYNYT-KETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARN
   SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVOWFAREGSAFITLSASVF
  SILAIAIERHVAIAXVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACST
  VLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRS------SHADMAAPOTLA
   Gaps
                       353
   352
                14;
  Length 381;
   Length 383;
   291 RSRDLRREVLRPLQCWR-PGVGVQGR-RRGGTPGHHLLPLRSSSS 333
  Query Match 46.9%; Score 847; DB 2; Length 38:
Best Local Similarity 48.7%; Pred. No. 7.9e-62;
Matches 168; Conservative 60; Mismatches 103; Indels
  THEMREAFIRIISCCKCPNGDSAGKFKRPIIPGMEFSRSKSDNS
   DB 2;
   46.3%; Score 836.5;
                       301
   301
   15
   62
   75
  122
   135
  182
   195
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   Query Match
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a function
  A;Cross-references: UNIPROT:092633; UNIPARC:UP10000050403; GB:U80811; NID:g1857424; PID:
C;Superfamily: G protein-coupled receptor edg-1
  88
  252
   137
  94 ADFFAGLAYFYLMFNTGPNTRRLTVSTWLLRQGLIDTSLTASVANLLAIAIERHITVFRM 153
   197
   212
  245
  WLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVLRPLQC 305
  IVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVLRP 302
  253 IACWSPLFIILPLIDVACRVQACPILFKAQWFIVLAVLNSAMNPVIYTLASKEMRRAFFR- 311
  93
   Jysophosphatidic acid receptor - human
NiAlternate names: Edg2 protein
NiAlternate names: Edg2 protein
C;Species: Homo sapiens (man)
C;Species: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: JC5293
R;An, S.; Dickens, M.A.; Bleu, T.; Hallmark, O.G.; Goetzl, E.J.
B;Acchem: Biophys. Res. Commun. 231, 619-622, 1997
A;Title: Molecular cloning of the human Edg2 protein and its identification A;Reference number: JC5293; MUID:97224397; PMID:9070858
A;Contents: lung
A;Accession: JC5293
A;Actatus: nucleic acid sequence not shown
A;Wolecule type: mRNA
A;Residues: 1-364 <ANAA>
  melanocortin 3 receptor - mouse
C;Species: Mus musculus (house mouse)
C;Decies: Ann-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S43850; S37153
R;Desarnaud, F; Labbe, O.; Eggerickx, D.; Vassart, G.; Parmentier, M.
                                       SKKYIAFCISIFTAILVTIVILYARIYFLVKSSSRKVANHNNSERSMALLRTVVIVVSVF
  SDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVFSLLAIAIERHVAIAKV
   KLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTI
  FSII-LLAIVALYVRIYCVVR-----SSHADMAAPQ-----TLALLKTVTIVLGVFIVC
  AKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMA----APQTLALLKTVTIVLGVF
   AIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLY
   18 YNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARNSKFHSAMYLFLGNLAA
   Gaps
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   / Match 27.9%; Score 504; DB 2; Length 36 Local Similarity 34.3%; Pred. No. 8.6e-34; nes 116; Conservative 71; Mismatches 121; Indels
   LQCWRPGVGVQGRRRGGTPGHHLL-PLRS-SSSLERGMHMP 341
   LVC---NCLVRGRGARASPIQPALDPSRSKSSSNNSSHSP 349
  WRPGVGVQGRRRGGTPGHHLLPLRSSSSLER----GMH 339
  Best Local Sim.
Matches 116;
   133
  187
  193
  243
  312
   78
  213
   246
   306
127
   303
  138
   198
  Query Match
   RESULT
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   G protein-coupled receptor - human (5.5 pecies Homo sapiens (man) (5.5 Accession: JC5245 (Maraguchi, F.; Tokuda, M.; Hatase, O.; Brenner, S. Bacchem. Elophys. Res. Commun. 227, 608-614, 1997 (Arcession: JC5245 (Mulb.97032811; PMID:8878560 A; Arcession: JC5245 (Mulb.97032811; PMID:8878560 A; Accession: JC5245 A; Mulb.97032811; PMID:8878560 A; Arcession: JC5245 A; Arcession: JC
  G protein-coupled receptor Gpcr13 - mouse (fragment)
G protein-coupled receptor Gpcr13 - mouse (fragment)
G protein-coupled receptor Gpcr13 - mouse (fragment)
G;Speciaes Mus musculus (house mouse)
G;Speciaes Mus musculus (house mouse)
G;Accession: E48909
E;Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G Genomics 18, 175-184, 1993
A;Pitle: Identification, chromosomal location, and genome organization of mammalian G-px A;Reference number: A48909
A;Reference number: A48909
A;Accession: E48909
A;Accession: E48909
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-180 <WILN-
A;Residues: 1-180 <WILN-
G;Superfamily: G protein-coupled receptor edg-1
C;Keywords: G protein-coupled receptor
   ö
  7
  241
   180
   132
  61 SLLAIAIERQVALAKVKLYGSDKSCRMLMLIGASWLISLILGGESILGWNCLNKLEACST 120
   62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTFVQWFAREGSAFITLSASVF 121
   122 SLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACST 181
  67 AMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVFSLLAI 126
   9
   99
  18 LREHYQYVGKIAGRLKEASEGSTLT----TVLFLVICSFIVLENLMVLIAIWKNNKFHN 72
  14 VQEHYNYT-----KETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVARNSKFHS
  1 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGHVTLSLTPVQWFAREVSAFITLSASVF
   VLPLYAKHYVLCVVT1FS11LLA1VALYVR1YCVVRSSHADMAAPQTLALLKTVT1VLGV
  Gaps
   Gaps
                                       305 KMLNC---GVCVQPSGKFSRP---IMGAEFSTSKSDNSSHPNKDEPEYSPRETIV 353
   301 RPLQCWRPGVGVGVRRRGGTPGHHLLPLRSSSSLERGMHMPT--SPTFLEGNTVV 353
   ö
  22;
   Match 42.6%; Score 769; DB 2; Length 378; Local Similarity 47.5%; Pred. No. 1.9e-55; les 162; Conservative 56; Mismatches 101; Indels
   Length 180;
  10; Indels
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Pred. No. 4.8e-59;
5; Mismatches 10
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C,Superfamily: G protein-coupled receptor edg-1
C,Keywords: G protein-coupled receptor
  Query Match
Best Local Similarity 91.7%;
Matches 165; Conservative
   Query Match
Best Local Si
Matches 162;
  182
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melanocortin receptor 3 - human

Cispecies: 12-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 04-Sep-1998

Cidate: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 04-Sep-1998

Cidates: 12-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 04-Sep-1998

Cidates: 12-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 04-Sep-1998

Cidates: 1.: Konda, Y.: Tashiro, T.: Shimoto, Y.: Miwa, H.: Munzert, G.: Watson, S.J.: D.

J. Biol. Chem. 268, 9246-8250, 1993

A;Title: Molecular cloning of a novel melanocortin receptor.

A;Reference number: A46647; MUID:93216807; PMID:8463333

A;Accession: B46647

A;Accession: B46647

A;Molecule type: nucleic acid
  G protein-coupled receptor 3 - human
NyAlternate names: G protein-coupled receptor GPR3; orphan G-protein-coupled receptor ACC (Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1995 #sequence revision 03-Mar-1995 #text_change 09-Jul-2004
C;Accession: A55689; S58521; C55733
R;Iismaa, T.P.; Kiefer, J.; Liu, M.L.; Baker, E.; Sutherland, G.R.; Shine, J. A;Title: Isolation and chromosomal localization of a novel human G-protein-coupled recept A;Reference number: A55689; MUID:95213036; PMID:7698767
   12;
  183
   191
  240
           249 CQVVWRHAHQIALQQHCLAPPHLAATRKGVGTLAVVLGTFGASWLP-FAIY-----CVVG 302
   123
  134
   226
   286
  241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHY -- XFAVSTLNSLLNPVIYTWRSRDLR -- 296
   287 VFIFCWAPFFHLVLIITCPTNPYCTCYTAHFNTYLVLIMCNSVIDPLIYAFRSLELRNT 346
  81
   135 AKVKLYGSDKSCR-MLLLIGASWLPSLVLGGLPILGWNCLGHLEACSTVLPLY--AKHYV
  184 FYALRYHSIMTVRKALTILVAIWV-------CCG---VCGVVFIVYSESKWVI
  192 LCVVTIFSIILLAIVALYVRIYCVVR-----SSHADMAAPQTLALLK---TVTIVLG
   262 -HSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREV-LRPLQCWRPGVGVQGR 315
  32 SRQVASAFI-----VILCCAIV--VENLLVLIAVARNSKFHSAMYLFLGNLAASDLL
  82 AGVAFVANTLL----SGSVTLRLTPVQWFAR--EGSAFITLSASVFSLLAIAIERHVAI
  303 SHEDPAVY-TYATLLPATYNSMINPIIYAFRNQEIQRALWLLLCGCFQSKVPFRSR 357
  Gaps
   53;
  Length 360;
  Indels
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A;Cross-references: UNIPARC;UPI00001789CB
A;Note: sequence extracted from NCBI backbone (NCBIP:129161)
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   A,Cross-references: GDB:138780
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C,Superfamily: melanocortin receptor
   Query Match 19.3%;
Best Local Similarity 33.4%;
Matches 102; Conservative 4
   A,Status: preliminary
A;Molecule type: DNA; mRNA
   297 -REVL 300
  FREIL 351
  A; Gene: GDB: MC3R
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   Grotein-coupled receptor 6 - human
C;Species: Homo sapiens (man)
C;Accession: I65990
R;Helber, M.; Docherty, J.M.; Shah, G;; Nguyen, T.; Cheng, R.; Heng, H.H.Q.; Marchese, A
DNA Cell Biol. 14, 25-35, 1995
A;Tile: Isolation of three novel human genes encoding G protein-coupled receptors.
A;Reference number: I53033; MUID:95134353; PMID:7832990
A;Reference number: I5590
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;References: UNIPROT:P46095; UNIPARC:UP100000DA4A; GB:L36150; NID:g598156; PIDN:
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A;Cross-references: GDB:371713; OMIM:600553
A;Cross-references: GBS:GRA
A;Map position: 6q21-6q21
C;Superfamily: melanocortin receptor
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Biochem. J. 299, 367-373, 1994
A;Title: Molecular cloning, functional expression and pharmacological characterization A;Title: Molecular cloning, functional expression and pharmacological characterization A;Reference number: S43850; MUID:94226597; PMID:8172596
A;Status: preliminary
A;Molecula type: DNA
A;Residues: 1-323 <DES>
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   11;
  13;
  |:|| : | || || || : :|
77 VLLCVSGTVIAGENALVVALIASTPALRTPMFVLVGSLATADLLAGCGLILHFVFQYLVP 136
   YVRIYCVVR-----SSHADMAAPQTLALLK---TVTIVLGVFIVCWLPAFSILLLDY 257
  SVTLRLTPVQWFAREGSAFITLSASVFSLLAIAIERHVAIAKVKLYGSDKS-CRMLLLIG 153
  154 ASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSIILLAIVALYVRIY 213
   214 CVVRSSHAD------MAAPQTLALLK---TVTIVLGVFIVCWLPAFSILLLDYACPV- 261
  93
   41 VILCCA---IVVENLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTL---LSG 94
   VILCCAIV--VENLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLL----S
   LIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLY--AKHYVLCVVTIFSIILLAIVAL
  36;
   267 TCPTNPYCICYTAHFNTYLVLIMCNSVIDPLIYAFRSLELRNTFKEIL 314
  Length 323;
   ACPVHSCPILYKAHY -- XFAVSTLNSLLNPVIYTWRSRDLR --- REVL 300
  Length 362;
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  19.3%; Score 349; DB 2; 34.1%; Pred. No. 4.1e-21;
  Best Local Similarity 34.11
Matches 101; Conservative
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  44
   94
  104
  209
   258
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  137
  Query Match
  Best Loc
Matches
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S40454
G protein-coupled receptor GPCR21 - mouse
C;Species: Mus musculus (house mouse)
   Local Similarity
  A;Gene: MC3-R
C;Superfamily:
C;Keywords: G p
   163
  268
  41
   95
  263
   Query Match
   Matches
  RESULT 14
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A;Residues: 1-330 <IIS>
A;Residues: 1-330 <IIS>
A;Cross-references: UNIPROT: P46089; UNIPARC: UPI0000001624; GB:L32830; GB:L32831; NID:g60
R;Eggerickx, D; Denef, J.F.; Labbe, O.; Hayashi, Y.; Refetoff, S.; Vassart, G.; Parment
Biochem. J. 309, 837-843, 1995
A;Title: Molecular cloning of an orphan G-protein-coupled receptor that constitutively a
A;Reference number: S58521
A;Retaus: preliminary; not compared with conceptual translation
A;Residues: Unipart; not compared with conceptual translation
A;Residues: Unipart; not compared with conceptual translation
A;Residues: UNIPARC: UPI0000001624; GB:R83956; NID:g1061125; PIDN:CAAS8787.1; PID
R;Rarchees, A; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui, I
Genomics 23, 609-618, 1994
A;Reference number: A55733; MUID:95154831; PMID:7851889
A;Recession: C5573
A;Retaus: preliminary
A;Rocession: C5573
A;Residues: 1-292 <WAR>
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A;Residues: UNIPARC: UPI000016A113; GB:U13668; NID:g577416; PIDN:AAA64594.1; PID:
C;Genetics:
A;Gene: GDB:GPR3
A;Cross-references: UNIPARC: UPI000016A113; GB:U13668; NID:g577416; PIDN:AAA64594.1; PID:
C;Genetics:
A;Gene: GDB:GPR3
A;Cross-references: UNIPARC: UPI000016A113; C;Genetics:
A;Gene: GDB:GPR3
A;Cross-references: UNIPARC: UPI000016A113; C;Genetics:
A;Genetics:
A;Geneti
  Risons, Z.H.; Young III, W.S.; Brownstein, M.J.; Bonner, T.I.
FEBS Lett. 351, 375-379, 1994
Aritie: Molecular cloning of a novel candidate G protein-coupled receptor from rat brain Aritie: molecular cloning of a novel candidate G protein-coupled receptor from rat brain Arecession: S48697, MUID:94364507; PMID:8082799
Arcession: S48697

   11;
   92 LSGSVTLRLTPVQWFAREGSAFITLSASVFSLLAIAIERHVAIAKVKLYGSDKS-CRMLL 150
   CIGSAEMSLVLV-----GVLAMAFTASIGSLLAITVDRXLSLYNALTYYSETTVTRTYV 155
   156 MLALVWGGALGLGLLPVLAWNCLDGLTTCGVVYPLSKNHLVVLAIAFFMVFGIMLQLYAQ 215
  91
   probable G protein-coupled receptor protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S48697
R;Song, Z.H.; Young III, W.S.; Brownstein M.T. Barnar T.
   38 AFIVILCCA---IVVENLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFV---ANTL
  151 LIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSI--ILLAIVAL
   209 YVRIYCVVRSSHADMAAPQTLAL------LKTVTIVLGVFIVCWLPAFSILLLDY
   Gaps
   36;
  ACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVLRPLQC 305
  Length 363;
  Length 330;
   Query Match 19.2%; Score 347; DB 2; Length 33:
Best Local Similarity 33.3%; Pred. No. 5.4e-21;
Matches 96; Conservative 49; Mismatches 107; Indels
  Query Match
18.9%; Score 340.5; DB 2;
Best Local Similarity 34.7%; Pred. No. 2e-20;
Matches 96; Conservative 51; Mismatches 95;
  102
   RESULT 12
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12;

Gaps

35;

Indels

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melanocortin receptor 3 - rat
melanocortin receptor 3 - rat
melanocortin receptor 3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A48254; S36636
B;Roselli-Rehfuss, L.; Mountjoy, K.G.; Robbins, L.S.; Mortrud, M.T.; Low, M.J.; Tatro, J
B;Roselli-Rehfuss, L.; Mountjoy, K.G.; Robbins, L.S.; Mortrud, M.T.; Low, M.J.; Tatro, J
A;Title: Identification of a receptor for gamma melanotropin and other proopiomelanocort
A;Reference number: A48254; MUID:94022273; PMID:8415620
A;Accession: A48254
A;Accession: A48254
A;Accession: A48254
A;Accession: A233 cROS
A;Residues: 1.323 cROS
A;Residues: 1.323 cROS
A;Crose-references: UNIPROT:P32244; UNIPARC:UPI000012ED4C; EMBL:X70667; NID:g396551; PID
A;Crose-references: UNIPROT:P32244; UNIPARC:UPIno0012ED4C; EMBL:X70667; NID:g396551; PID
A;Note: submitted to the EMBL Data Library, January 1993
A;Note: submitted to the EMBL Data Library, January 1993
A;Note: in Genbank entry RRNC3RA, release 113.0, the source is designated as Rattus ratt
   153
   103
  209
  --SLIVAI------WVCCG---ICGVMFIVYSESKWIVCLITWFFAMVLLMGTLY 207
   210 VRIYCVVR-----SSHADMAAPQTLALLK---TVTIVLGVFIVCWLPAFSILLLDYA 258
  267
  213
   CVVRSSHAD------MAAPQTLALLK---TVTIVLGVFIVCWLPAFSILLLDYACPVH 262
  94 GSVTLRLTPVQWFAR--EGSAFITLSASVFSLLAIAIAERHVAIAKVKLYGSDKSCRMLLL 151
94
  44 VFLALGIVSLMENILVILAVVRNGNLHSPMYFFLLSLLQADMLVSLSNSLETIMIVVINS
  208 IHMFLFARLHVQRIAALPPADGVAPQQHSCMKGAVTITILLGVFIFCWAPFFLHLVLIIT
   152 IGASWLISLVLGGLPILGWNCLGHLEACSTVLPLY--AKHYVLCVVTIFSIILLAIVALY
  SVTLRLTPVQWFAREGSAFITLSASVFSLLAIAIERHVAIAKVKLYGSDKS-CRMLLLIG
VILCCA---IVVENLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLLS---G
   154 ASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSIILLAIVALYVRIY
   41 VILCCAIV--VENLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLL----S
   CPVHSCPILYKAHY - - XPAVSTLNSLLNPVIYTWRSRDLRREVLRPLOCWRPGVGV 312
   Gaps
   41;
   DB 2; Length 323;
   Superfamily: melanocortin receptor;
Keywords: G protein-coupled receptor; transmembrane protein;
   Indels
  304 SQEDPAIY-TYATLLPATYNSMINPIIYAFRNQEIQR 339
   S--CPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRR 297
  th 18.7%; Score 338.5; DB 2; Similarity 32.1%; Pred. No. 2.6e-20; 95; Conservative 56; Mismatches 104;
```

223

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144 HSRSLRCRPSYHFIGSLAVADLLGSVIFVYSFVDFHVFHRKDSPNVFLFKLGGVTASFTA 203
   119 SVFSLLAIAIERHVAI----AKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLG 174
   261 LQSVCSDIFPLIDETYLMFWIGVTSVLLFIVYAXMYILWKAHSHAVRMIQRGTQKSIII 320
  ------AAPQTLALLKTVTIVLGVFIVCWLPAFSILLLDYACPVHSCPILYK 269
  175 HLEACSTVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADM------
  270 AHYXFA--VSTLNSLLNPVIYTWRSRDLR 296
  completed: December 4, 2005, 06:52:57
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   A33117
Canabinoid receptor CB1 - rat
canabinoid receptor CB1 - rat
canabinoid receptor CB1 - rat
canabinoid receptor Rattus norvegicus (Norway rat)
C; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
R; Matsuda, L.A.; Lolait, S.J.; Brownstein, M.J.; Young, A.C.; Bonner, T.I.
Nature 346, 561-564, 1990
A; Reference number: A33117; MUD: 90332039; PMID: 2165569
A; Residues 1-473 eMar>
A; Molecule type: mRNA
A; Residues: 1-473 eMar>
A; Residues: D: Carillon, C: Kaghad, M: Calandra, Eranslation
A; Residues: Preliminary; not compared with conceptual translation
A; Residues: UNIPARC:UPI00001768D8
A; Residues: UNIPARC:UPI00001768D8
C; Keywords: G protein-coupled receptor; glycoprotein; membrane protein
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S40454
K;Saeki, Y; Usono, S.; Mizuno, R.; Nishimura, T.; Fujimura, H.; Nagai, Y.; Yanagihara, T
FEBS Lett. 336, 317-322, 1993
A;Title: Molecular cloning of a novel putative G protein-coupled receptor (GPCR21) which
A;Reference number: S40454
A;Accession: S40454
A;Accession: S40454
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-330 <ABA:
A;Accession: S40594: MID:94085630; PMID:9600025C17; GB:D21062; NID:9455487; PIDN:
C;Superfamily: melanocortin receptor
C;Keywords: G protein-coupled receptor; phosphoprotein; transmembrane protein
  8
   C | | : | | | : | | | : | | | | : | | | | : | | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | : | | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
  LIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSI -- ILLAIVAL 208
  | | : : | : | | | | | : | 84 NKSLSSFKENEENIQCGENFMDMECFMILNPSQQLAIAVLSLTLGTFTVLENLLVLCVIL 143
  LSGSVTLRLTPVQWFAREGSAFITLSASVFSLLAIAIERHVAIAKVKLYGSDKS-CRMLL 150
  YVRIYCVVRSSHADMAAPQTLAL------LKTVTIVLGVFIVCWLPAFSILLLDY 257
  216 ICRIVC----RHAQQIALQRHLLPASHYVATRKGIATLAVVLGAFAACWLPFTVYCLLGD 271
   RNSKFH-SAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSA 118
   38 AFIVILCCA---IVVENLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFV---ANTL 91
   12 NKVQEHYNYTKETLETQE-----TTSRQVASAFI-VILCCAIVVENLLVLIAVA 59
  Gaps
   36;
  Query Match 16.7%; Score 302; DB 2; Length 473; Best Local Similarity 28.0%; Pred. No. 3.7e-17; Matches 92; Conservative 58; Mismatches 129; Indels 50;
   A----DSPRLY-TYLTLLPATYNSMINPVIYAFRNQDVQK-VLWAICC 313
  ACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVLRPLQC 305
   Length 330;
   / Match 18.7%; Score 338; DB 2; Length 330
Local Similarity 32.3%; Pred. No. 3e-20;
Nes 93; Conservative 50; Mismatches 109; Indels
  Query Match
Best Local Si
Matches 93;
   92
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   US-10-084-507B-17
1806
1 MGSLYSEYLNPNKVQEHYNY......LERGMHMPTSPTFLEGNTVV 353
   2443163
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
   Total number of hits satisfying chosen parameters:
  2443163 segs, 439378781 residues
   Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  OM protein - protein search, using sw model
  Gapop 10.0 , Gapext 0.5
   geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2003as:*
geneseqp2003s:*
geneseqp2004s:*
  geneseqp1980s:*
   Minimum DB seq length: 0
Maximum DB seq length: 200000000
   A_Geneseq_21:*
1: qeneseqp198
  4
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  December
  BLOSUM62
  ..........
  Post-processing:
   Perfect score:
  Scoring table:
  Sequence:
  Searched:
   Database
  Run on:
   Title:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description         | Aay28288 Predicted | Aay49904 Human EDG | Aay28289 EDG-4 ami | Aab18889 Amino aci | Abp59285 Human Edg | Abb98694 Human End | Abu08813 Human EDG | Abp82010 Human sph | Adc40485 Protein o | Add11247 Human EDG | Add90760 Human Edg | Adh57161 Human end | Adj62652 Human end | Ado29293 Human GPC | Ado57997 Human EDG | 2 Human  | Adp88359 Human EDG | Aay49905 Human EDG | Add11249 Human EDG | Adu92079 Human end | Aab03966 Murine ED | Aar58712 Fragment |          | Aay05492 Human EDG |
|-----------|---------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|----------|--------------------|
| SUMMARIES | a                   | AAY28288           | AAY49904           | AAY28289           | AAB18889           | ABP59285           | ABB98694           | ABU08813           | ABP82010           | ADC40485           | ADD11247           | ADD90760           | ADH57161           | ADJ62652           | AD029293           | AD057997           | AD022422 | ADP88359           | AAY49905           | ADD11249           | ADU92079           | AAB03966           | AAR58712          | AAW01663 | AAY05492           |
|           | DB                  | 7                  | ~                  | ~                  | m                  | 9                  | 9                  | 9                  | 9                  | 7                  | 7                  | 7                  | œ                  | œ                  | ω                  | œ                  | œ        | œ                  | N                  | 7                  | σ                  | m                  | ~                 | 7        | 7                  |
|           | Length              | 353                | 353                | 353                | 353                | 353                | 353                | 353                | 353                | 353                | 353                | 353                | 353                | 353                | 353                | 353                | 353      | 353                | 353                | 353                | 353                | 352                | 352               | 352      | 352                |
|           | *<br>Query<br>Match | 9.                 | 6.6                | 8.                 | 6.8                | 6.                 | 9.9                | 98.9               | 98.9               | 98.9               | 98.9               | 98.9               | 98.9               | 6.                 | 98.9               | 98.9               | 98.9     | 98.9               | 98.7               | 98.7               | 97.2               | 90.3               | 0.06              | 0.       | 0.0                |
| •         | Query<br>Matcl      | 66                 | 66                 | 66                 | õ                  | 86                 | 8                  | ñ                  | 5                  | 6                  | ல்                 | ñ                  | 9                  | ñ                  | ñ                  | 5                  | õ        | õ                  | ñ                  | ñ                  | ģ                  | á                  | ñ                 | 90       | 8                  |
|           | Score               | 1804               | 1804               | 1803               | 1787               | 1787               | 1787               | 1787               | 1787               | 1787               | 1787               | 1787               | 1787               | 1787               | 1787               | 1787               | 1787     | 1787               | 1783               | 1783               | 1755               | 1631.5             | 1625.5            | 1625.5   | 1625.5             |
|           | Result<br>No.       |                    | 7                  | 3                  | 4                  | S                  | 9                  | 7                  | 80                 | 0                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16       | 17                 | 18                 | 19                 | 20                 | 21                 | 22                | 23       | 24                 |

A novel isolated lysolipid (LL) receptor/EDG receptor (EDG-4). The LL/EDG receptors are involved in an inflammatory response signaling pathway and an apoptotic signaling pathway. They can be used for identifying agonists or antagonists of NF-kB or IL-8 modulated EDG or LL receptors. Agonists can be used for upregulation of an inflammatory process condition or immune response. Antagonists can be used for the downregulation of an

Claim 7; Fig 16A; 120pp; English.

|   | Rat HZ18, | LPA recep | Rat lysop | Rat Endot | Human sph | Rat endot | Rat Prote | Murine En | Mouse GPC | Human sec | Chimeric | Human 7 t | Human rep | Human tes | Human 7 t | Chimeric | Chimeric | Chimeric | Human Edg | Arrestin | Chimeric |
|---|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|----------|----------|----------|-----------|----------|----------|
|   |           | 5         |           |           |           |           | 7         | ñ         |           | 6         | 5        | ñ         |           | 5         |           | ₫        | <u>.</u> | <u>ق</u> | 6         | 7        | 9        |
|   | Aaw87790  | Aau00305  | Abu07712  | Abb98696  | Abu61816  | Adp88361  | Add48927  | Abb98695  | Ado29294  | Adp29509  | Abp59289 | Adg15135  | Aam96680  | Abb96585  | Adg15162  | Abp59281 | Abp59280 | Abp59279 | Abg75679  | Ado28787 | Adx44606 |
|   | AAW87790  | AAU00305  | ABU07712  | ABB98696  | ABU61816  | ADP88361  | ADD48927  | ABB98695  | AD029294  | ADP29509  | ABP59289 | ADG15135  | AAM96680  | ABB96585  | ADG15162  | ABP59281 | ABP59280 | ABP59279 | ABG75679  | AD028787 | ADX44606 |
|   | N         | 4         | 9         | 9         | 7         | œ         | 7         | 9         | œ         | œ         | 9        | 4         | 4         | 4         | 4         | ø        | 9        | 9        | ស         | 80       | σ        |
| 1 | 352       | 352       | 352       | 352       | 352       | 352       | 353       | 352       | 352       | 377       | 372      | 269       | 274       | 274       | 274       | 384      | 384      | 391      | 362       | 362      | 362      |
|   | 90.0      | 90.0      | 90.0      | 90.0      | 90.0      | 90.0      | 90.0      | 89.8      | 89.8      | 83.6      | 79.3     | 52.4      | 52.4      | 52.4      | 52.4      | 47.6     | 47.5     | 47.5     | 47.3      | 47.3     | 47.3     |
|   | 1625.5    | 1625.5    | 1625.5    | 1625.5    | 1625.5    | 1625.5    | 1625.5    | 1622.5    | 1622.5    | 1509.5    | 1432     | 947       | 947       | 947       | 947       | 860.5    | 858.5    | 858      | 854.5     | 854.5    | 854.5    |
|   | 25        | 26        | 27        | 28        | 29        | 30        | 31        | 32        | 33        | 34        | 35       | 36        | 37        | 38        | 39        | 40       | 41       | 42       | 43        | 44       | 45       |

## ALIGNMENTS

RESULT 1

```
New isolated lysolipid/EDG receptor useful in the treatment of asthma and rheumatoid arthritis.
  EDG-4; polypeptide; receptor; inflammation; amino acid; G protein; lysolipid; immune response.
   Gupta AK;
   Vyas TB,
   Predicted polypeptide product from human EDG-4 cDNA
   Kooshesh F,
  /label= unknown
/note= "encoded by YTT"
  (ALLX ) ALLELIX BIOPHARMACEUTICALS INC.
   Location/Qualifiers
      AAY28288 standard; protein; 353 AA
   Peters D,
  97US-0070185P.
98US-0080610P.
98US-0109885P.
   98WO-CA001195.
                                      (first entry)
   Kamboj R,
  WPI; 1999-430392/36.
   Misc-difference
  Homo sapiens
   30-DEC-1998;
  WO9935259-A1
                                      12-OCT-1999
   30-DEC-1997;
   03-APR-1998;
25-NOV-1998;
  15-JUL-1999.
   Munroe DG,
                      AAY28288;
AAY28288
```

antagonists can also be used for controlling apoptosis in a cell
comprising the LL/EDG receptor. A diagnostic test for aberrant expression
of HEBG-4 can accelerate diagnosts and proper treatment of abnormal
conditions of e.g. the heart, kidney, lung and testis. Specific examples
of conditions in which aberrant expression of HEBG-4 may play a role
include adult respiratory distress, asthma, rheumatoid arthritis, stroke,
conditions in which aberrant expression of HEBG-4 may play a role
include adult respiratory distress, asthma, rheumatoid arthritis, stroke,
concurranma, Alzheimer's disease, endotoxic shock, psoriasis,
cardiac ischemia, acute pancreatitis, septic shock, psoriasis of the
cyclosporine nephrotoxicity, HIV/AIDS, myelodysplasia, cirrhosis of the
cliver, and early diabetic glomerulopathy, as well as lung damage
collowing exposure to cigarette smoke, abestos or silica. HEDG-4
specific antibodies, inhibitors, ligands or their analogs can be used as
bloactive agents to treat inflammation or disease including viral,
bacterial or fungal infections, allergic responses, mechanical injury
associated with trauma, hereditary diseases, lymphoma or carcinoma, or
cother conditions which activate the genes of kidney, lung, heart,
cyclymphoid or tissues of the nervous system The agonists and inflammatory process condition or immune response. 8888888888888888888888

Sequence 353 AA;

ö 120 180 180 240 240 VFIVCWLPARSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300 9 9 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLBACS 1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV FSLLAIAIBRHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG Gaps RPLOCWRPGVGGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353 ö 99.9%; Score 1804; DB 2; Length 353; 100.0%; Pred. No. 1.3e-177; ive 0; Mismatches 0; Indels Local Similarity 100. 19 61 121 181 181 241 241 301 301 Query Match Best Loca Matches ð g ઠે 셤 δ ద g ò 셤 8 g ò

AAY49904 standard; protein; 353 AA

(first entry) 28-JAN-2000

Human EDG family H218 protein.

Human; EDG family; H218; transmembrane receptor protein; diagnosis; therapy; bacterial; fungal; viral; infection; HIV; cancer; diabetes; obesity; anorexia; bulimia; asthma; Parkinson's disease; hypotension; acute heart failure; hypertension; urinary retention; osteoporosis; angina pectoris; mycoardial infarction; stroke; ulcer; asthma; allergy; benign prostatic hypertrophy; migraine; vomiting; psychotic; neurological disorder; dyskinesia. 

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Homo sapiens

WO9954351-A1

28-OCT-1999

is used for diagnosing disease or its susceptibility in a subject related with expression or activity of H218 by determining the presence or absence of mutation in the polymuclectide encoding H218 in the genome of the subject and/or analysing for the presence of 4218 expression in sample derived from the subject. It is also used for treating subjects in need of enhanced activity or inhibition of H218 by administering an agonist or antagonist respectively. H218 can be used to treat abnormal conditions such as bacterial, fungal and viral infections, particularly H1V-1 or 2, cancers, diabetes, beeity, anoraxia, bullimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, urinary retention, osteoporosis, angina pectoris, myocardial infarction, erroke, ulcers asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic, neurological disorders and dyskinesias can be treated. The H218 polymucleotide can also used for obtaining control of migration probes and primers for isolating full-length clones encoding H218. The difference in cDNA or genomic sequence between affected and unaffected individuals is determined to identify mutation causing the disease. It is also valuable for chromosome identify mutation causing the disease. It is also valuable for chromosome identify mutation control receptors through standard receptor binding techniques and also control or exceptors through standard receptor binding techniques and also present sequence is a human EDG family protein designated H218. H218 Novel human transmembrane receptor protein for use in treatment and ä Tsui Mooney JL, Li X, <u>.</u> Lane (SMIK ) SMITHKLINE BEECHAM CORP. Claim 1; Page 29; 49pp; English. 98US-00150650 99WO-US008099 98US-0082776P DJ, Elshourbagy N, diagnosis of disease. WPI; 1999-633972/54. N-PSDB; AAZ32488 14-APR-1999; 23-APR-1998; 03-SEP-1998; polypeptides Bergsma 

Sequence 353 AA;

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120 120 180 180 240 240 300 241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300 9 9 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS VFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVL 1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 181 TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG 1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS Gaps ó, Length 353; Indels Score 1804; DB 2; Pred. No. 1.3e-177; 0; Mismatches 1; 99.9%; Query Match Best Local Similarity 99.7° Matches 352; Conservative 121 181 241

61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

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RESULT 4
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   A novel isolated lysolipid (LL) receptor/EDG receptor (EDG-4). The LL/EDG receptors are involved in an inflammatory response signaling pathway and an apoptotic signaling pathway. They can be used for identifying agonists or antagonists of NR-kB or IL-8 modulated EDG or LL receptors. Agonists or antagonists of NR-kB or IL-8 modulated EDG or LL receptors. Agonists or immune response. The agonists and inflammatory process condition or immune response. The agonists and inflammatory process condition or immune response. The agonists and inflammatory process condition or immune response. The agonists and engine and proper treatment expression of the EDG-4 can accelerate diagnosis and proper treatment of abnormal conditions of e.g. the heart, Kidney, lung and testis. Specific examples of conditions in which aberrant expression of HEDG-4 may play a role include adult respiratory distress, asthma. Theumatorid arthritis, stroke, neurotrauma, Alzheimer's disease, andotoxic shock, atherosclerosis, cardiac ischemia, acute pancreatiis, septic shock, psoriasis, acute cyclosporine nephrotoxicity, HIV/AIDS, myelodysplasia, cirrhosis of the liver, and early diabetic glomerulopathy, as well as lung damage cyclosporine nephrotoxicity, HIV/AIDS, myelodysplasia, cirrhosis of the cyclosporine agents to treat inflammation or disease including viral, bacterial or fungal infections, allergic responses, mechanical injury associated with trauma, hereditary diseases, lymphoma or carcinoma, or other conditions which activate the genes of kidney, lung, heart, lymphoid or tissues of the nervous system
   New isolated lysolipid/EDG receptor useful in the treatment of asthma and
   receptor; inflammation; amino acid; G protein;
  Gupta AK;
   Score 1803; DB 2; Length 353;
Pred. No. 1.7e-177;
1; Mismatches 1; Indels 0
   EDG-4 amino acid sequence encoded by clone pC3-hEDG4#36.
   Vyas TB,
   Peters D, Kooshesh F,
  (ALLX ) ALLELIX BIOPHARMACEUTICALS INC.
  AAY28289 standard; protein; 353 AA.
   Claim 7; Fig 16B; 120pp; English.
   99.8%;
  98US-0080610P.
   98WO-CA001195.
   97US-0070185P.
  BDG-4; polypeptide; receptc
lysolipid; immune response.
   (first entry)
   Kamboj R,
  rheumatoid arthritis.
  WPI; 1999-430392/36.
   Local Similarity
  Sequence 353 AA;
  Homo sapiens.
  WO9935259-A1
   30-DEC-1998;
  30-DEC-1997;
  03-APR-1998;
25-NOV-1998;
   15-JUL-1999.
   12-OCT-1999
  Munroe DG,
  AAY28289;
   Query Match
RESULT 3
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The present sequence represents an Edg polypeptide. The specification describes Edg4 and Edg5 polypeptides. The Edg4 gene is located on chromosome 19pl2. The Edg polypeptides are receptors for 1ycophospholipids and sphingolipids, such as lysophosphatidic acid (LPA) and sphingosine 1-phosphate (SIP). The Edg receptor proteins are used for diagnosing an LPA or SIP mediator condition an individual. Edg4 and Edg5 polypeptides can be used in screening assays designed to determine the Effects of a candidate bioactive agent on the expression and activity of Edg4 and Edg5 polypeptides, and the function of LPA and SIP. Nucleotide sequences encoding Edg-4 and Edg-5 are useful a hybridisation probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. Nucleic acids which encode Edg4 or Edg5 or their modified forms can also be used to generate either transgenic animals or knock out animals.
180
                240
  240
   VFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
  241 VFIVCWLPAFSILLIDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
  Novel human polypeptide receptors for lysophospholipids and sphingolipids, native human Edg4, Edg5, mutant of Edg4 comprising extended polypeptide tail, used to screen agents that affect LPA and S1P
   TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
   301 RPLQCWRPGVGVGGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353
   Edg4; Edg5; lysophospholipid receptor; sphingolipid receptor; S1P; lysophosphatidic acid; LPA: sphingosine 1-phosphate; gene therapy.
  Amino acid sequence of the human Edg5 polypeptide.
   AAB18889 standard; protein; 353 AA
   Claim 13; Fig 3; 67pp; English.
  23-MAR-2000; 2000WO-US007649.
   99US-00274752.
  08-FEB-2001 (first entry)
   (REGC ) UNIV CALIFORNIA
   WPI; 2000-638230/61.
  An S;
  N-PSDB; AAA96163.
   in gene therapy
   WO200056135-A2.
   23-MAR-1999;
   Homo sapiens
  28-SEP-2000.
  activities.
  Goetzl EI,
 121
   AAB18889;
  301
  181
   241
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Sequence 353 AA;

120

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Gaps

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1 MGSLYSBYLNPNKVQBHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR

1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR

Matches 351; Conservative

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NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTFVQWFAREGSAF1TLSASV

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  120
  120
   180
  240
   240
  300
   180
  The present invention relates to Edg receptors (ABPS9277-ABPS9290). The Edg receptors, are useful in a high-throughput screening assay to identify compounds that bind to or modulate the activity of the polypeptide, in calcium mobilisation assays, binding assays, detection of cAMP formation, or in reporter gene techniques
   VFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
   9
  9
   New chimeric Edg receptor, useful in high-throughput screening assays, comprises extracellular and transmembrane domains of a first Edg receptor, and a chimeric intracellular domain of a second Edg receptor.
   FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
   VFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVL
  MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
  NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV
   FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
  TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
                         Gaps
   RPLOCWRPGVGGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353
                         ;
  Length 353
                        Indels
 Score 1787; DB 3;
Pred. No. 7.5e-176;
0; Mismatches 3;
  Spencer JV;
   Disclosure; Page 19; 71pp; English.
   Ź
  ABP59285 standard; protein; 353
vuery Match 98.9%;
Best Local Similarity 99.2%;
Matches 350; Conservative
  10-JUL-2002; 2002WO-US022346
   11-JUL-2001; 2001US-00904099
   entry)
  'n,
  (first
  Munning
  WPI; 2003-221718/21.
   Human Edg5 receptor
  Sequence 353 AA;
  WO2003006503-A1.
   (CERE-) CERETEK.
   Homo sapiens
   Edg;
   polypeptide,
cAMP formati
  10-MAY-2003
  23-JAN-2003
   Shankar G,
   63
   61
  121
  121
  181
   181
   241
   241
  301
  301
  ABP59285;
   Human;
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   180
  240
   240
   120
   120
   180
   300
  241 VFIVCWLPAFSILLLDYACPVHSCPILYXAHYFFAVSTLNSLLNPVIYTWRSRDLRREVL 300
   The present invention relates to methods for screening for preventives or remedies for proliferative glomerular nephritis, depending on the inhibitory effect on Endothelial Differentiation Gene, Edg-5, activation. The method is especially useful for screening preventives or remedies for IgA nephritis. The present sequence is human Edg-5, which was used in the method of the invention
   9
  9
  FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
   181 TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
  1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
   NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV
  61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVOWFAREGSASITLSASV
                                       MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
  TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
   VFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL
               Gaps
  Screening drugs for preventing or treating (mesangial) proliferative glomerular nephritis, based on inhibiting activation of Edg-5 for particularly Edg-5 receptor antagonists.
   301 RPLQCWRPGVGVGRRRVGTPGHHLLPLRSSSSLERGWHMPTSPTFLEGNTVV 353
  RPLOCWRPGVGGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353
               ö
  Human; nephrotropic; proliferative glomerular nephritis;
Endothelial Differentiation Gene; Edg-5; IgA nephritis.
               Indels
 7.5e-176;
ches 3;
  Human Endothelial Differentiation Gene, Edg-5.
              Mismatches
 No.
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 Pred.
   2
   Tsujimoto
   Claim 3; Page 44; 59pp; Japanese.
  ABB98694 standard; protein; 353
              ô
  (NNSH ) NIPPON SHINYAKU CO LTD
   26-MAR-2001; 2001JP-00088018.
06-SEP-2001; 2001JP-00270551.
  25-MAR-2002; 2002WO-JP002828
99.2%;
  (first entry)
               Conservative
   s,
   Katsuma
  WPI; 2003-018956/01.
Similarity
   N-PSDB; ABQ81030.
  WO200277642-A1.
  10-JAN-2003
  Homo sapiens
   Takagaki K,
              350;
   03-OCT-2002
                                       _
   ABB98694;
   61
   121
   241
  181
  301
 Best Local
               Matches
   ABB98694
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Sequence 353 AA;

98.9%; Score 1787; DB 6; Length 353;

Query Match

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  The invention discloses method for identifying a compound that modulates lymphocyte activation/migration. The method comprises contacting an EDG G-protein coupled receptor (GPCR) family polypeptide, or its fragment or a
  300
   Human; lymphocyte activation; lymphocyte migration; EDG-5; G-protein coupled receptor; GPCR; lymphocyte; T cell receptor; E cell receptor; D69; gene therapy; asthma; allergy; autoimmune disease; multiple sclerosis; scleroderma; pernicious anaemia; IDDM; insulin-dependent diabetes mellitus; tissue transplant; graft-versus-host disease; inflammation; infection.
   identifying lymphocyte modulator activation/migration, by contacting an SDG G-protein coupled receptor polypeptide or cell having the polypeptide with compound and determining chemical/phenotypic effect of compound on
   180
   240
   TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIXCVVRSSHADMAAPQTLALLKTVTIVLG 240
  VFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
  9
  241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVL
  61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV
   121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
   1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
  1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
   NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV
   FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
   TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
   Gaps
   301 RPLQCWRPGVGVGRRRVGTPGHHLLPLRSSSSLERGWHMPTSPTFLEGNTVV 353
  301 RPLQCWRPGVGVQGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353
   ;
0
   Jiang
Length 353;
  Indela
   H,
  Zhao 1
Score 1787; DB 6;
Pred. No. 7.5e-176;
0; Mismatches 3;
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  Pardo J,
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  Disclosure; Fig 2; 70pp; English.
   ABU08813 standard; protein; 353
   18-APR-2001; 2001US-0284763P
   03-OCT-2001; 2001US-00971228
  Chu P,
98.9%;
   11-AUG-2003 (first entry)
                          Local Similarity 99.2
nes 350; Conservative
   RIGE-) RIGEL PHARM INC.
  WPI; 2003-340852/32.
  Human EDG-5 protein.
  Masuda E,
   US2002155512-A1
  Homo sapiens
   24-OCT-2002
  Liao XC,
   61
  ABU08813;
   121
   181
Query Match
  RESULT 7
ABU08813
ID ABU08813
XX ABU0 XX
XX B Huma
XX Huma
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cerat countising the playpeptine of lies fragment with the compound, and determining the chemical/phenotypic effect of the compound upon the call also disclosed are methods for modulating tymphocyte activation or a subject, by administering to the subject a therapeutically effective amount of an identified compound, an EDG polypeptide or a concleic acid encoding an EDG, or its fragment, and for screening for modulators of lymphocyte activation, by transfecting into lymphocytes a converse converse activation of lymphocyte activation by detecting the level of EDGs cell surface expression and rescuing coDNas that modulate converse conver
   G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; ADS; cancer; immunological-related cell proliferation; disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
  120
  61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
   PSLIAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS 180
   240
  240
  300
   FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS 180
  9
   241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSRDLRRREVL
  VFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL
  1 MGSLYSBYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
  NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV
   TVLPLYAKHYVLCVVTIPSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
  1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
  Gaps
  comprising the polypeptide or its fragment with the compound,
  RPLQCWRPGVGVQGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353
  ö
   Length 353;
  Indels
   Human sphingolipid receptor Edg5 protein SEQ ID NO:508.
   Score 1787; DB 6;
Pred. No. 7.5e-176;
0; Mismatches 3;
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  ABP82010 standard; protein; 353
   98.9%;
99.2%;
   04-MAR-2003 (first entry)
   Best Local Similarity 99.2
Matches 350; Conservative
   Sequence 353 AA;
  61
   121
   121
  181
  301
  181
  241
   Query Match
   ABP82010
  RESULT
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The invention relates to a novel method for gene expression analysis by collective quantitative analysis of the expression of a number of genes to identify those that are promoted or inhibited in a given cell or tissue. The genes are preferably gene families such as the G protein gene family. The methods may be used in treatment of cancers, including prostate, ovarian, stomach, bladder, breast, and cancer of the intestines. EDG-1 and EDG-2 receptor agonists and antagonists may be used in the treatment and prevention of atheroscelerosis, myocardial infarction, infarct or ischaemic disease of the brain. This sequence represents a protein of human EDG-5 of the invention.
  181 TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG 240
   241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYPFAVSTLNSLLNPVIYTWRSRDLRREVL 300
   G protein coupled receptor; tyrosine oxidase receptor family; ion channel gene family; cancer; EDG-1; EDG-2 receptor; atherosclerosis; myocardial infarction; infarct; ischaemic disease; GPCR; human; EDG-5.
  1 MGSLYSBYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
   VFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL
  1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
   RPLOCWRPGVGVQGRRRVGTPGHHLLPLRSSSSLERGMIMPTSPTFLEGNTVV 353
   301 RPLQCWRPGVGVQGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV
   Method for gene expression analysis for treatment of cancers.
   Length 353;
  gene expression analysis; collective quantitative analysis;
   Indels
  Fujii R,
  <u>ب</u>
   Score 1787; DB 7;
Pred. No. 7.5e-176;
); Mismatches 3;
  Fukusumi S,
   Disclosure; SEQ ID NO 46; 261pp; Japanese.
   Ź
  Arai T,
, Ogi K;
  ;
0
  ADC40485 standard; protein; 353
   14-DEC-2001; 2001JP-00382053.
21-FEB-2002; 2002JP-00045104.
15-MAY-2002; 2002JP-00140111.
18-NOV-2002; 2002JP-00333769.
  13-DEC-2002; 2002WO-JP013097.
   98.9%;
99.2%;
   (TAKE ) TAKEDA CHEM IND LTD.
  Kawamata Y,
   18-DEC-2003 (first entry)
   Query Match
Best Local Similarity 99.2'
Matches 350; Conservative
  Kobayashi M,
   Protein of human EDG-5.
   2003-533023/50.
   N-PSDB; ADC40486
   Sequence 353 AA;
   WO2003052096-A1
  Matsumura F,
  Homo sapiens.
  26-JUN-2003
  ADC40485;
  Hinuma S,
   301
   RESULT 9
  ADC40485
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  caids. Also described: (1) an assay for the detection of a particular of acids. Also described: (1) an assay for the detection of a particular of acids. Also described: (1) an assay for the detection of a particular of protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (1) can be used as GPCR modulators and in the becapy. The antisquence of GPCR, and in the production of specific antibody against a particular GPCR, and in the production of specific antibody against a particular GPCR, and in the production of specific cantibody against a particular GPCR. The antisquence of appendix and antibodies are useful for disposing and designing the presence or absence of corresponding GPCRs. The antisquence peptides for GPCRs and antibodies are useful for disposing and designing the greating immune-related dispose, immunological-related disposes, call reacting immune disposes, immunological-related cell proliferative chiesases, or autoimmune dispose, e.g. AIDS, Alzheimer's dispose, catherosis, bacterial, fungal, protozoan or viral infections, osteoporosis, cancer, cardiomyopathy, chronic and acute disposes, parkinson's dispose, multiple sclerosis, pain, psoriasis, cancer, cardiomyopathy, chronic and acute consension, schizophrenia, dementia, mental retardation, memory consections, cancer in which GPCRs are involved. The antibodies may be used in immunosasays and immunodiagnosis. ABZ42523 to ABZ42869 encode committed of the property of the prop
   ö
   120
  180
  240
  New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
   FSILLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS 180
  9
  9
hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
   The present invention describes antigenic peptides (I) comprising: (a)
  MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
   NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV
   FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
  TULPLYAKHYULCVVTI FSI ILLAI VALYVRI YCVVRSSHADMAAPQTLALLKTVTI VLG
   1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
   Gaps
   ö
   Length 353;
  3; Indels
   Score 1787; DB 6;
Pred. No. 7.5e-176;
  0; Mismatches
  exemplification of the present invention
   Disclosure; Fig 1; 523pp; English.
  (LIFE-) LIFESPAN BIOSCIENCES INC.
   Brown JP;
  19-DEC-2000; 2000US-0257144P.
   19-DEC-2001; 2001WO-US050107
  Query Match
Best Local Similarity 99.2%;
Matches 350; Conservative
  Burmer GC, Roush CL,
   WPI; 2003-046718/04.
   autoimmune diseases.
   N-PSDB; ABZ42860.
  Sequence 353 AA;
   WO200261087-A2
   Homo sapiens.
  08-AUG-2002
   61
  19
   121
  121
   181
                            ulcer.
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Gaps

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The present invention describes a method for identifying an increase in risk for Type II diabetees mellitus and/or venous thrombosis/pulmonary embolism, comprising determining the presence of amino acid exchange at position 266 from Val to Ala in the EDG5 protein. Also described: (1) a preventing type II diabetes and/or venous thrombosis/pulmonary embolism, where a cell or cell extract is used that contains EDG5 with the amino acid exchange, or the variation in the nucleotide sequence of EDG5 protein or the EDG5-286-AA; (2) a method for adapting the dosage of the pharmacceutical described above by testing the human cell for the presence of EDG5 protein or the EDG5-286-AA; (2) a method of selecting parients who will respond type II diabetes and/or venous thrombosis/pulmonary embolism by testing the probe of the respective
   Identifying an increase in risk for Type II diabetes mellitus and/or venous thrombosis/pulmonary embolism comprises determining in a probe the presence of amino acid exchange at position 286 from Val to Ala in the
   300
  240
  240
NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
   II diabetes mellitus; venous thrombosis; pulmonary embolism; EDG5; V286A; antidiabetic; thrombolytic; gene therapy; human.
   TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIXCVVRSSHADMAAPQTLALLKTVTIVLG
  VFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVL
                   NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV
  FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
  TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
   VPIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL
  ŝ
   301 RPLQCWRPGVGVQGRRRVGTPGHHLLPLRSSSSLERGWHWPTSPTFLEGNTVV 353
   RPLQCWRPGVGVQGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353
  Ricard
  Jacobs M, Deleuze J,
  Example 2; SEQ ID NO 3; 21pp; English.
  Siegler K,
  ADD11247 standard; protein; 353 AA
   (AVET ) AVENTIS PHARMA DEUT GMBH
  Human EDG5 protein SEQ ID NO:3
   07-APR-2003; 2003WO-EP003569
  09-APR-2002; 2002EP-00007879
  (first entry)
  Kozian D, Kostenis E,
   2003-804314/75.
  N-PSDB; ADD11248
   WO2003085130-A1.
  protein.
   Homo sapiens.
  01-JAN-2004
  16-OCT-2003
                               61
  121
   121
  181
   181
  241
   301
   Mace S;
  Type
  EDGS
  ADD11247
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patient for the presence of EDG5 with the amino acid exchange, or the variation in the nucleotide sequence of EDG5 protein or the EDG5-286-AA; and (4) a test kit for testing the presence of the amino acid exchange, or the variation in the nucleotide sequence of EDG5 protein or the EDG5-286-AA. EDG5 has antidiabetic and thrombolytic activities, and can be used in gene therapy. The methods are useful for identifying an increase in risk for type II diabetes mellitus and/or thrombosis/pulmonary embolism, and for screening pharmaceuticals useful for treating type II diabetes mellitus and/or venous thrombosis/pulmonary embolism. The methods are also useful for adapting the dosage of a pharmaceutical useful for treating the above diseases. The methods are useful for sequence represents who will respond to the pharmaceutical. The present sequence represent invention.
  120
  180
  240
   300
   120
  241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVL 300
   9
   receptor; human; Edg5 receptor; gastrointestinal disorder; cardiovascular disorder; hypertension; diabetes; respiratory disorder; asthma; immune disorder; cognitive disorder; memory disorder; obesity; pain; psychotic behaviour; affective disorder; migraine; cancer; AIDS; wound healing; ischaemia-reperfusion injury-related disease.
   VFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL
  NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV
   FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
   TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
  1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
  1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
   Gaps
  RPLQCWRPGVGVQGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353
  ;
0
  Length 353;
   Indels
  98.9%; Score 1787; DB 7;
99.2%; Pred. No. 7.5e-176;
iive 0; Mismatches 3;
   Ź
   ADD90760 standard; protein; 353
   2002US-00228762
  (first entry)
  Matches 350; Conservative
  Human Edg5 receptor.
  Local Similarity
   Sequence 353 AA;
   US2003130493-A1
   Homo sapiens.
   26-AUG-2002;
   29-JAN-2004
  10-JUL-2003
  ADD90760;
   61
  61
   121
  121
   181
  181
   241
  301
   301
   Query Match
   RESULT 11
   ADD90760
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   ઠે
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  g
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   ઠે
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99US-00253998.

22-FEB-1999; 16-JUL-1999;

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(WILS/)

(HUAN/) BORO/) SALO/)

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This invention relates to a novel method for identifying an increase in risk for type II diabetes mellitus, venous thrombosis, pulmonary embolism or a combination thereof. Specifically, it refers to a the endothelial differentiation gene 5 (EDG5) located on chromosome 19913.2, which encodes a G protein coupled receptor protein. The present invention describes an immunochemically reactive labelled antibody based kit that can be used to identify the Val286Ala variation in the EDG5 protein encoded by a single nucleotide polymorphism. Furthermore, this allele encoding the V286A variant represents a genetic marker that can be useful for preventative treatments of the aforementioned diseases, as well as for adapting drug dosage for patients, for drug screening purposes or for patient selection in phase or clinical studies. This polypeptide sequence is the human EDG5 protein of the invention.
  Identifying an increase in risk for type II diabetes mellitus, venous thrombosis, pulmonary embolism or its combination in subject by determining whether amino acid residue at position 286 of BDG5 protein is
  61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV
   1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
  61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV
   1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
   121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
   121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
  G protein coupled receptor; EDG5; type II diabetes mellitus; venous thrombosis; pulmonary embolism; endothelial differentiation
Human endothelial differentiation factor 5 (EDGS) protein SeqID 3.
   98.9%; Score 1787; DB 8;
99.2%; Pred. No. 7.5e-176;
iive 0; Mismatches 3;
  Example 2.4; SEQ ID NO 3; 10pp; English.
  Siegler K,
  60
  21-MAR-2003; 2003US-00393870
   09-AUG-2002; 2002US-0402305P.
   3est_Local Similarity 99.2
4atches 350; Conservative
  Kostenis E,
  WPI; 2004-060183/06.
  KOZIAN D.
KOSTENIS E.
  SIEGLER K.
   JACOBS M.
DELEUZE J.
   RICARD S.
  N-PSDB; ADH57162
  Sequence 353 AA;
  US2003219808-A1
   ŝ
   MACE
  27-NOV-2003
  Kozian D,
  Query Match
   (JACO/)
(DELE/)
(RICA/)
(MACE/)
   alanine.
   ŝ
  (KOST/
  (SIEG/
   Mace
   Homo
    SXCCCCCCCCCCCXSXLLLLXXBAXBABABABXXXLLXXBXAXBX
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  The invention relates to an isolated nucleic acid encoding a mammalian Edg7 receptor. The mammalian Edg7 receptor proteins and nucleic acid encoding the proteins are useful for diagnosing and treating an abnormality associated with the activity of the mammalian Edg7 receptors, cdiabetes, respiratory disorder, asthma, immune disorder, hypertension, disorder, memory disorder, obssity, pain, psychotic behaviour, affective disorder, migraine, cancer, AIDS, wound healing, or ischaemia-reperfusion injury-related diseases. The nucleic acids and proteins are also useful for developing and designing drugs with higher specificity and fewer side effects. The nucleic acid such an attisense oligonucleotides concoling mammalian Edg7 receptors and antisense oligonucleotides complementary to the nucleic acid sequences. The methods are also useful for identifying agonists and antisense oligonuclectics. The present so requence represents the amino acid sequence of the human Edg5 receptor.
   ö
   mammalian
  FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS 180
   FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS 180
   VPIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
   241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIXTWRSRDLRREVL 300
  New mammalian Edg7 receptor proteins and nucleic acids encoding mammaliar
Edg7 receptors, useful for diagnosing and treating an abnormality
associated with the activity of the mammalian Edg7 receptor, e.g. asthma,
  9
  MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
  1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
   NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV
  TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
   Gaps
   Nagorny
  RPLQCWRPGVGVQGRRRVGTPGHHLLPLRSSSSLERGMIMPTSPTFLEGNTVV 353
  RPLQCWRPGVGGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353
   .
0
  Length 353;
   Wilson A,
   Score 1787; DB 7; Length 3
Pred. No. 7.5e-176;
0; Mismatches 3; Indels
   Salon JA,
   Disclosure; SEQ ID NO 19; 64pp; English.
   Borowsky BE,
  ADH57161 standard; protein; 353 AA.
  98.9%;
99.2%;
  Query Match
Best Local Similarity 99.2
Matches 350; Conservative
  Bonini JA, Huang LY,
                   HUANG L Y.
BOROWSKY B E.
SALON J A.
WILSON A.
  WPI; 2003-829581/77
   migraine or cancer.
BONINI J A.
  NAGORNY R.
  Seguence 353 AA;
   61
   61
  121
  301
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121

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181 181 241

Ricard S;

Deleuze J,

Jacobs M,

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Indele

Length 353;

180 240 240

TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG

181 181

ò

(first entry)

25-MAR-2004

ADH57161;

301

RESULT 12

Gaps

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3; Indels

Mismatches

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Conservative

350;

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Matches
   RESULT 14
   AD029293
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  The invention relates to a compound 8-80 nucleobases in length targeted to, and which specifically hybridises with a nucleic acid molecule encoding endothelial differentiation gene 5 (EDG5, a G protein coupled receptor, involved in development, wound healing, tissue regeneration, callular proliferation, apoptosis, cancer, angiogenesis and infibite the expression of EDG5, i.e. is an antisense (AS) oligonucleotide. Also included are a composition comprising the compound and a carrier or diluent and a method for screening an antisense compound (by contacting a preferred target region of a nucleic acid compounds comprising at least an 8-nucleobase portion that is complementary to the preferred target region and selecting for one or more candidate antisense compounds that inhibit the expression of a nucleic acid encoding EDG5). The compound, composition and methods are useful for treating a disease or condition associated with EDG5, such as a hyperproliferative disorder,
 241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
                241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVL 300
  developmental disorder or a disease or condition arising from aberrant apoptosis. They are also useful in research and diagnostics for modulating the expression of EDGS. Experimental protocols are described but no results are given. The present sequence is the human EDGS protein.
   endothelial differentiation gene 5; EDG5; G protein-coupled receptor; development; wound healing; tissue regeneration; cellular proliferation; apoptosis; cancer; angiogenesis; inflammation; hyperproliferative disorder; developmental disorder.
  New antisense oligonucleotide targeted to nucleic acid encoding endochelial differentiation sphingolipid G-protein-coupled receptor 5, for treating cancer, developmental disorder or a condition arising from aberrant apoptosis.
  301 RPLQCWRPGVGVQGRRRVGTPGHHLLPLRSSSSLERGWHMPTSPTFLEGNTVV 353
   RPLOCWRPGVGVQGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353
  Score 1787; DB 8; Length 353; Pred. No. 7.5e-176;
  Human endothelial differentiation gene 5 protein.
  antisense gene therapy,
  Disclosure; Page 31-32; 50pp; English.
   Ź
   ADJ62652 standard; protein; 353
  98.9%;
99.2%;
  09-AUG-2002; 2002US-00215821.
  09-AUG-2002; 2002US-00215821
   (first entry)
   (ISIS-) ISIS PHARM INC.
   2004-179674/17.
  Query Match
Best Local Similarity
  N-PSDB; ADJ62544.
  receptor;
  Sequence 353 AA;
   US2004029274-A1
   sapiens
   06-MAY-2004
  12-FEB-2004
   301
   ADJ62652;
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KW g protein-coupled receptor; GPCR; drug screening; diagnosis;

KW transgenic mouse; neurological disorder; adrenal gland disorder;

KW colon disorder; intestinal disorder; cardiovascular disorder;

KW muscular disorder; blood disorder; immune disorder; bone disorder;

joint disorder; liver disorder; nutritive disorder; cancer;

KW kidney disorder; liver disorder; pung disorder; breast disorder;

KW disorder; terns disorder; pancreas disorder; spleen disorder;

KW kin disorder; thyroid disorder; pancreas disorder; spleen disorder;

KW phymus disorder; thyroid disorder; antiparkinsonian; antimanic;

KW CNS; central nervous system; respiratory; antidiarhoeic; antidiabetic;

W CNS; central nervous system; respiratory; antidiarhoeic; antidiabetic;

W charactological; antiulcer; antithyroid; antiallergic; anorectic;

M immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
   61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
   180
   240
  240
   VFIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
   9
 9
   1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
   TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG
1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR
   NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV
   FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS
   Novel mammalian G protein coupled receptors, useful for identifying
  RPLQCWRPGVGVQGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353
   Li F;
Zeng H;
   Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J,
Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D,
   AD029293 standard; protein; 353 AA
   Human GPCR EDG5, SEQ ID NO:394.
   09-SEP-2002; 2002US-0409303P. 09-APR-2003; 2003US-0461329P.
  09-SEP-2003; 2003WO-US028226.
   (first entry)
  WPI; 2004-390329/36
  (PRIM-) PRIMAL INC.
  N-PSDB; ADO29865.
  WO2004040000-A2
   29-JUL-2004
   Homo sapiens
   13-MAY-2004.
   Madisen L,
   241
  AD029293;
   61
  181
  241
   301
   121
   181
  301
  receptor
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compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.

12-AUG-2004 (first entry)

ADO57997;

Claim 151; SEQ ID NO 394; 542pp; English.

The invention relates to human and mouse G protein-coupled receptors

(GPCRs) and nucleic acids encoding them. The invention also relates to
sequences at least 90% identical to the GPCR proteins and nucleic acids
of the invention; methods of treating, preventing or diagnosing diseases
compounds useful in the treatment of GPCR-related diseases; a transgenic
compounds useful in the treatment of GPCR-related diseases; a transgenic
compounds useful in the treatment of GPCR-related diseases; a transgenic
compounds useful in the treatment of GPCR-related diseases; a transgenic
compounds useful in the treatment of GPCR-related diseases; cells derived
from the trassgenic mice; kits comprising several mice, each of which has
comprising a GPCR transgene or in an endogenous GPCR gene; cells derived
comprising a GPCR nucleic acid. The GPCR mucleic acids and proteins may
be used in the diagnosis, treatment or prevention of a wide variety of
invention further discloses variants of the GPCR polypeptides and vectors
comprising a GPCR nucleic acid. The GPCR mucleic acids and proteins may
be used in the diagnosis, treatment or prevention of a wide variety of
depression, diabetic neuropathy, Parkinson's disease or schizophrenia's
disorders of the adrenal gland; disorders (e.g., Alzheimer's disease,
disorders of the adrenal gland; disorders (e.g., angina, cardiac arrhythmia or
myccardial infarction); muscular disorders (e.g., autoimmune disorders of e.g.,
anaemia or leukaemia); immune disorders (e.g., autoimmune disorders of
competity, enzyme deficiency-related diseases or vitamin disorders or
diseases); and disorders (e.g., on turtitie, due content,
prostate, testis, skin, stomech, pancreas, spleen, thymus and
thyroid (e.g., cancers). The present sequence represents a GPCR of the
invention. Note: The full sequence data for this patent did not form part
contens, prostate, testis, skin, secondaria sequences.
The printed specification; those sequences.

Sequence 353 AA;

ò 180 240 300 VPIVCWLPAFSILLLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300 9 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG 241 VFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAVSTLNSLINPVIYTWRSRDLRREVL 1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAVAR FSLLAIAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACS TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG Gaps RPLQCWRPGVGVQGRRRGGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353 RPLQCWRPGVGVQGRRVGTPGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV 353 ć o Length 353; 3; Indels 98.9%; Score 1787; DB 8; 99.2%; Pred. No. 7.5e-176; iive 0; Mismatches 3; Matches 350; Conservative Query Match Best Local Similarity 61 121 121 181 181 241 301 셤 ò 유 셤 ò 셤 Š ద ò

comprises capanosing arseases such as a caraturbascular diseases, diseases in a mammal. The invention also comprises a pharmaceutical diseases in a mammal. The invention also comprises a pharmaceutical composition for the treatment of the diseases above comprising an EDG5 polyapeptide or which regulates the EDG5 polypeptide activity composition for the treatment of the diseases above comprising an EDG5 polyapeptide or which regulates the EDG5 polypeptide activity such as a small molecule, an RNA molecule, an antisense oligonuclectide, a polypeptide, an antibody, or a ribozyme; and preparation of a polypeptide, an antibody, or a ribozyme; and preparation of a polypeptide, an antibody, or a ribozyme; and preparation of a trianteriosclerotic, antisthmatic, antiarteriosclerotic, antisthmatic, antiarteriosclerotic, antisthmatic, antiarteriosclerotic, antisthmatic, antiarteriosclerotic, antiparkinsonian, antiulocer, cardiant, cerebroprotective, dermatological, gynecological, neuroprotective, cerebroprotective, dermatological, gynecological, neuroprotective, cerebroprotective, dermatological, gynecological, neuroprotective, cerebroprotective, dermatological, gynecological, neuroprotective, cerebroprotective, diseases, disorders of the gastroenterology system, cerebroprotective diseases, disorders of the gastroenterology system, cerebroprotective, diseases in a mammal. They are also useful for the regulation of EDG5 activity in a mammal having the disease.

Cardiovascular disease includes heart failure, myocardial infarction, ischaemia, arrhythmias, and atherosclerosis. Examples of disorders of the peripheral and central nervous gastrictis, gastric ulcers, and chronic pancreatitis. Examples of disorders of the peripheral and central or erproduction disorders are syphilis, genital warts, impotence, vaginitis, dermenta, and infartility. Disorders of the peripheral and central or erproduction disorders and infartalismor's diseases comples compensation or erproduction disorders and infartalismory diseases compensation or e

agents. The method comprises contacting a test compound with an endotherlial differentiation sphingolipid G-protein-coupled receptor 5 (EDGS) polypeptide or polymucleotide and detecting binding of the test compound, or determining EDGS polypeptide activity at a certain test compound concentration or in the absence of the test compound and at a different concentration of the test compound. The invention further comprises: diagnosing diseases such as a cardiovascular diseases,

The invention relates to a novel method for screening for therapeutic

Disclosure; SEQ ID NO 2; 119pp; English.

ADO57997 standard; protein; 353 AA. RESULT 15 ADO57997

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EDGS; cardiovascular disease; gastroenterology system; reproductive; peripheral; central nervous system; respiratory; analgesic; antiarrhythmic; antiarteriosclerotic; antiarthythmic; antiarteriosclerotic; antiarthatic; antibacterial; antiinfertility; antiinflammatory; antiparkinsonian; antiulcer; cardiant; cerebroprotective; dermatological; synecological; neuroprotective; nootropic; varucide; human.
   Screening for therapeutic agents, useful for treating e.g. respiratory disease, comprises contacting a test compound with endothelial differentiation sphingolipid G-protein-coupled receptor 5 polypeptide and
   endothelial differentiation sphingolipid; G-protein-coupled receptor
   ï.
  Summer
  31-OCT-2003; 2003WO-EP012122.
   13-NOV-2002; 2002EP-00025098.
                                    Human EDG5 receptor protein.
  (FARB ) BAYER HEALTHCARE AG.
   Golz S, Brueggemeier U,
  WPI; 2004-449580/42.
   detecting binding.
  N-PSDB; ADO57996.
  WO2004044587-A2
  Homo sapiens.
   27-MAY-2004.
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chronic obstructive pulmonary disease. The nucleotide sequences encoding EDG5 are useful as hybridization probes, in constructing oligomers for PCR, for chromosome and gene mapping, in the recombinant production of EDG5, in generating antisense DNA or RNA and in molecular biology techniques that have not yet been developed. EDG5 polypeptides are useful for immunising a mammal to produce polyclonal antibodies and for diagnostic purposes. This sequence represents the human EDG5 receptor protein of the invention.
                       888888888888
```

Sequence 353 AA;

ö Gaps ; 0 Score 1787; DB 8; Length 353; Pred. No. 7.5e-176; 3; Indels 0; Mismatches 98.9**%**; 99.2**%**; Query Match Best Local Similarity 99.2° Matches 350; Conservative

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180 121 181

RPLQCMRPGVGVQGRRRVGTPGHHLLPLRSSSSLERGMMPTSPTFLEGNTVV 353 RPLOCWRPGVGVGGRRRGGTPGHHLLPLRSSSSLERGWHMPTSPTFLEGNTVV 353 301

completed: December 4, 2005, 06:46:53 Search completed: Do Job time: 133 secs

